

PGN1

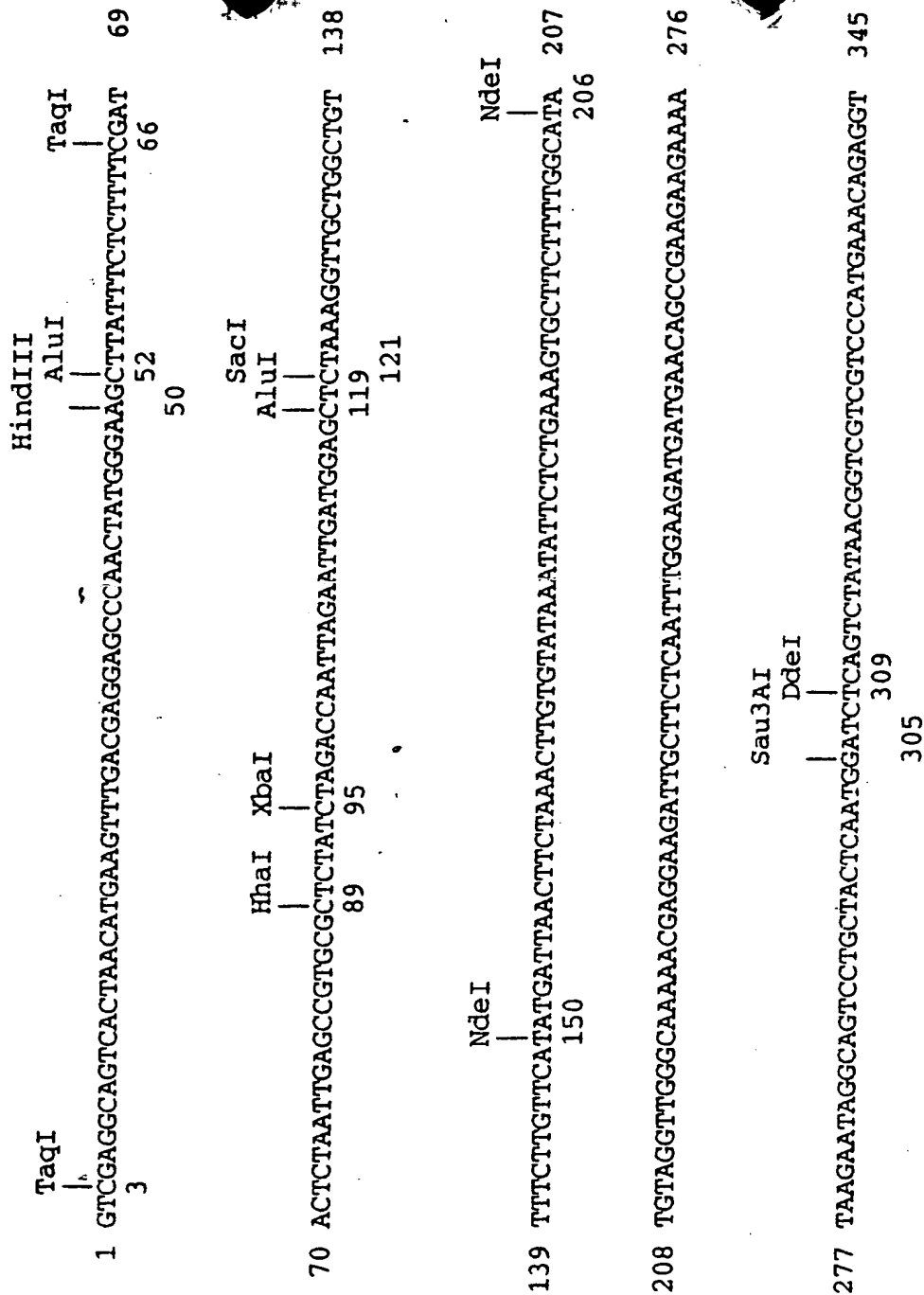


FIG. 1A

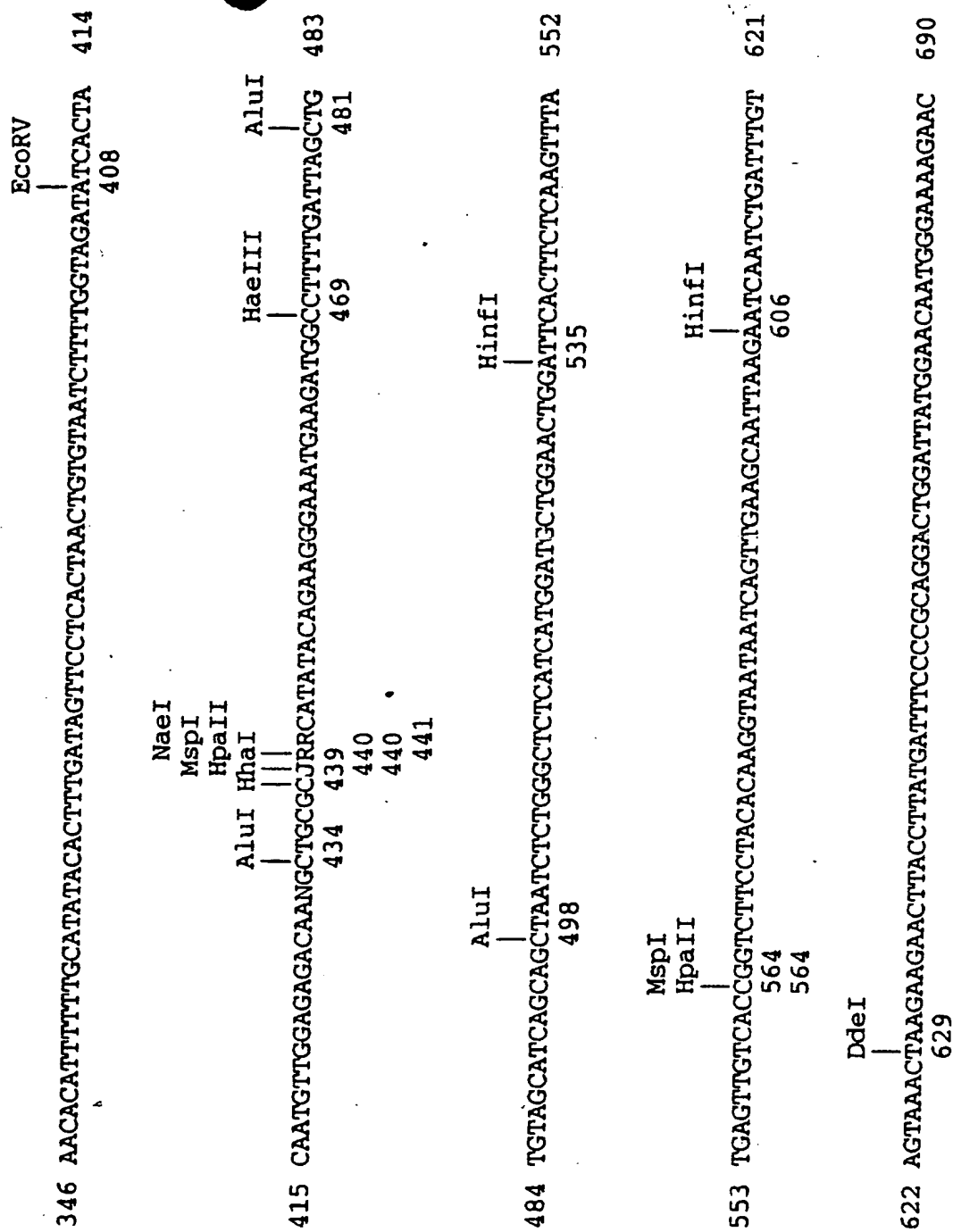


FIG. 1B

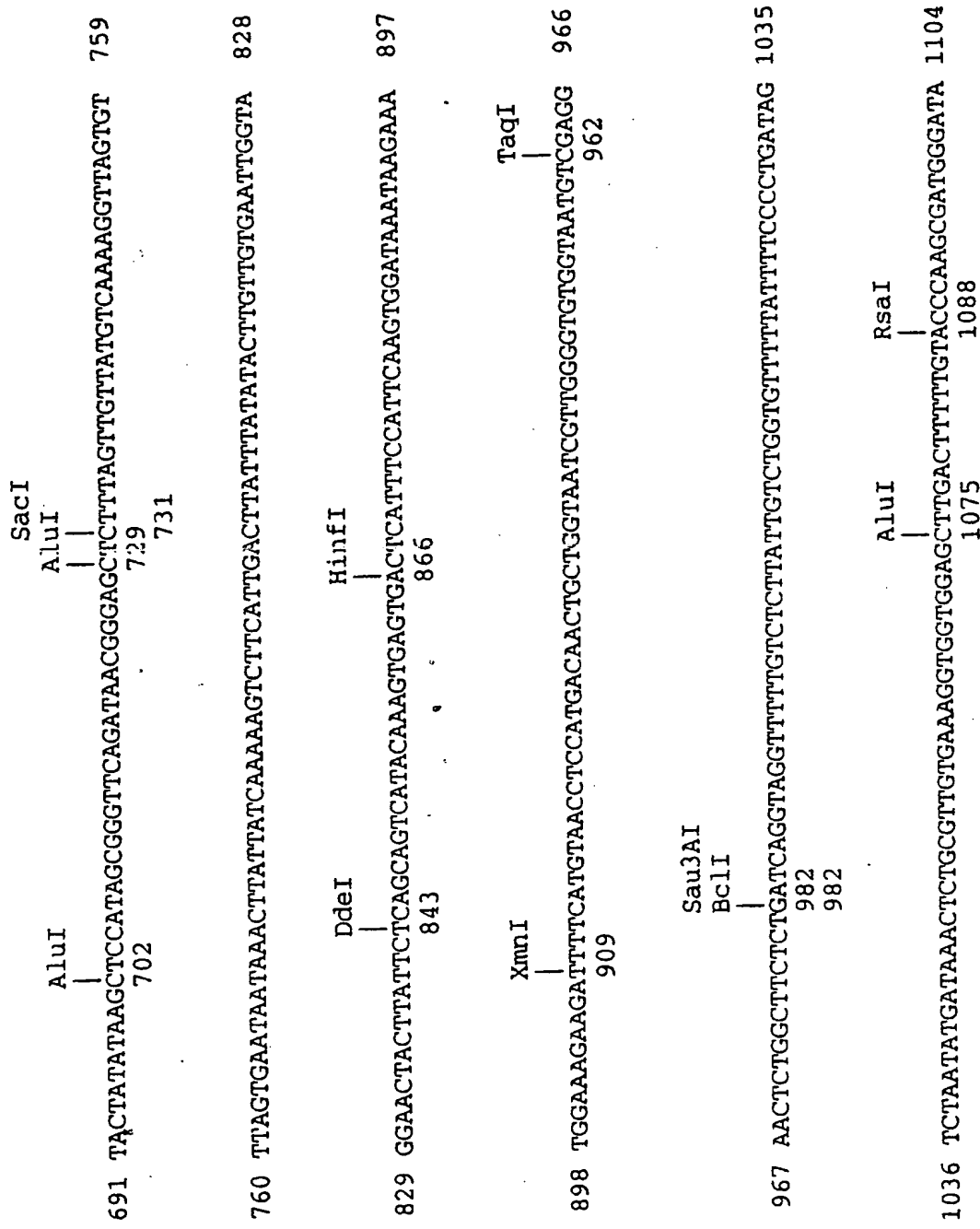


FIG. 1C

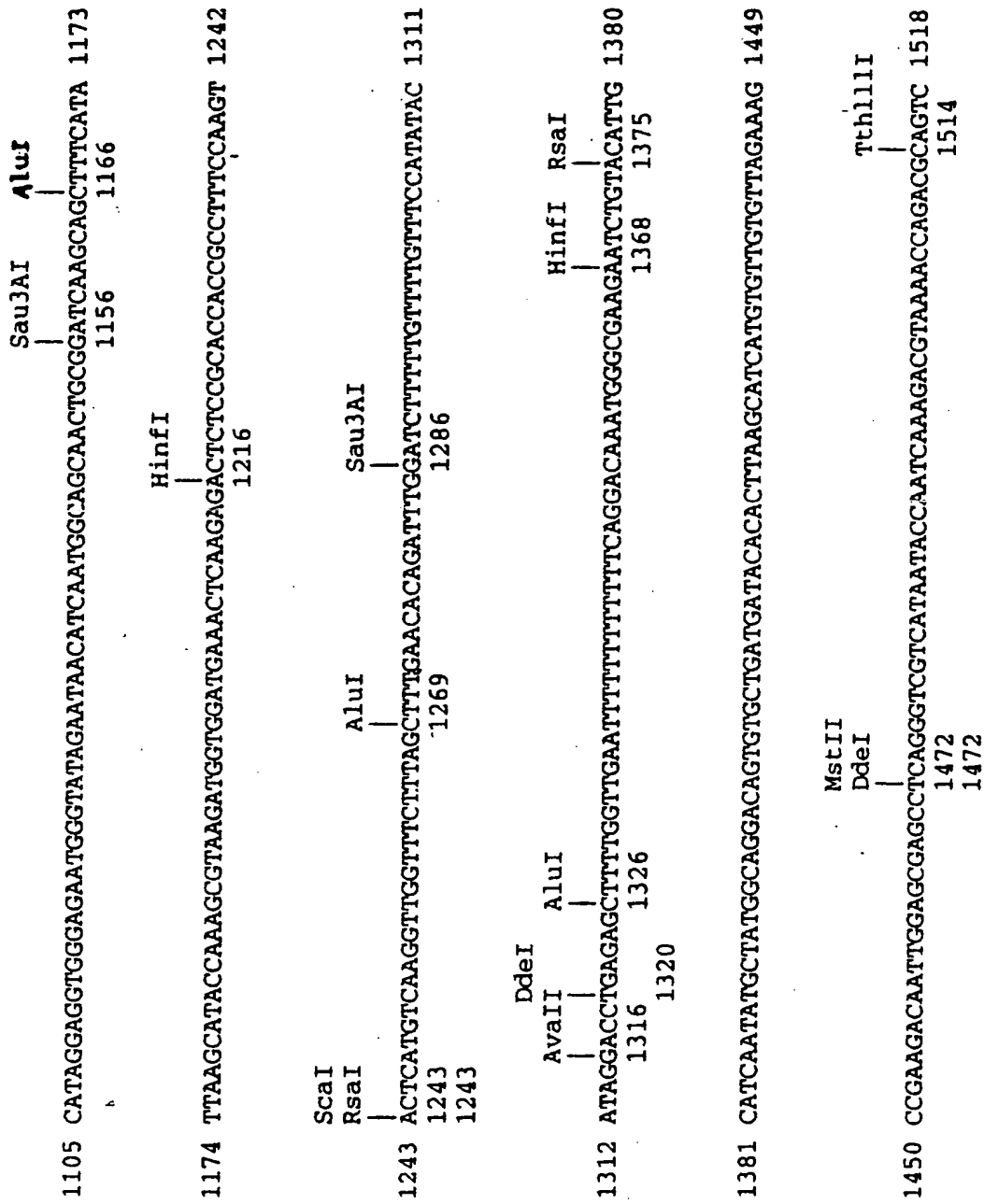


FIG. 1D

1519 TCCTTTGGTTGAATGTGATGAAAGGGATGTGTCTTGGTATGTATGTACGAGTAACAAAAGAGAAGATGCA 1587
RsaI | 1564

1588 ATTGAGTAGTAGAAAGATTTGAGAGCTTTTAAAGCCCTTCAAGTGTGTGCTTTTATCTTATTTGATATC 1656
AluI | DraI | EcoRV | 1654

1657 ATCCATTGCGTGTGTTTAATGCGTCTTTAGATAATGTTTCTGTCTTCTCAGTGTCTGAATATCTGAT 1725
DdeI | 1706

1726 AAGTGCAATGTGAGAAAGCCACACCAACCAAAATATTCAAATCTTATATATTTTAAATAATGTCTGAATCA 1794
TaqI | HinfI | 1790
1788

1795 CTCGGAGTTGCCACCTTCTGTGCCAATGTGTGCTGAATCTATCACAATAAAAAACATTTCTTCAAGGT 1863
HinfI | 1829

1864 AATGACTTGTGGACTATGTTCTGAAATTTCTCATTAAGTTTTTATTTTTTTGAAGTTTAAGTTTTTACCTTC 1932
EcoRI | 1887

FIG. 1E

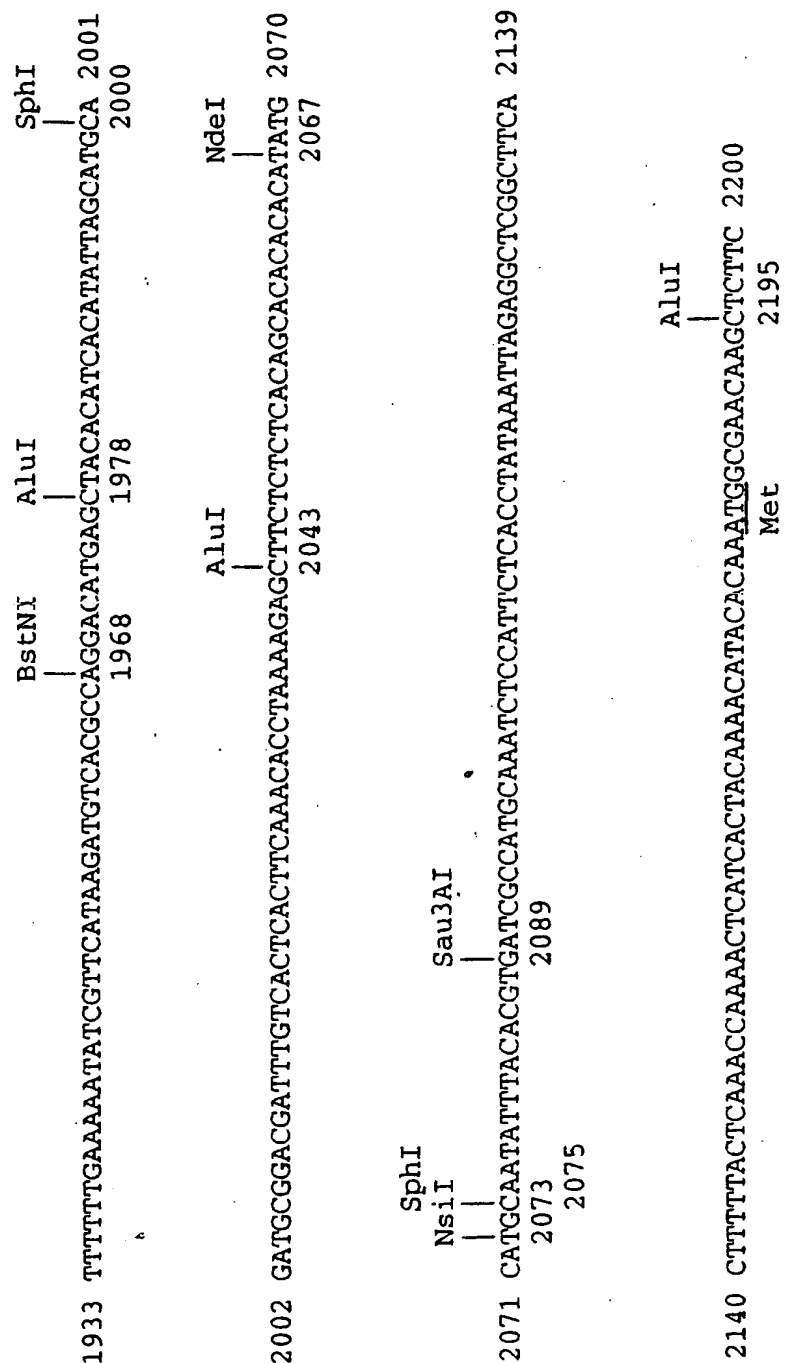


FIG. 1F

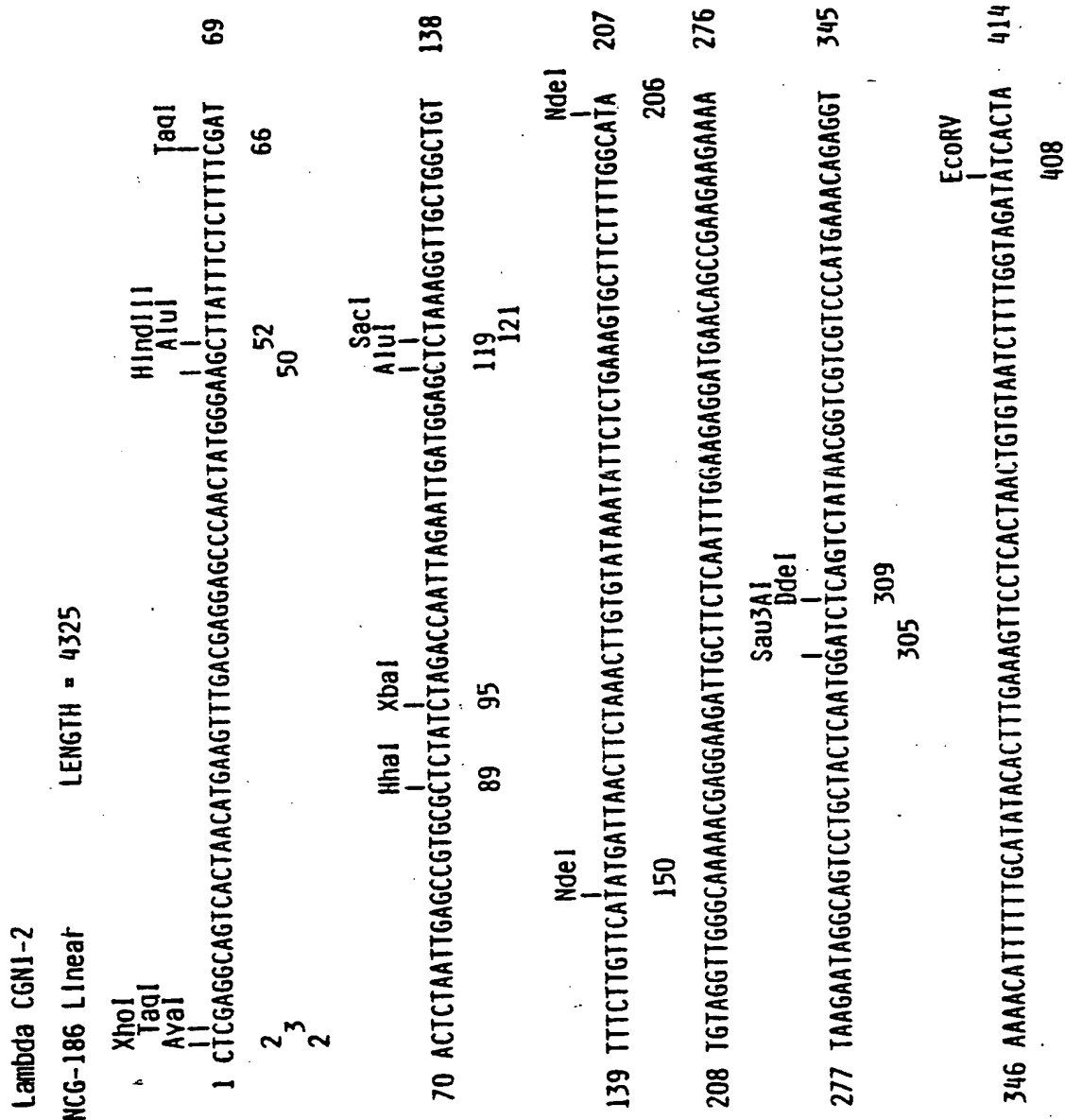


FIG. 2A

FIG. 2B



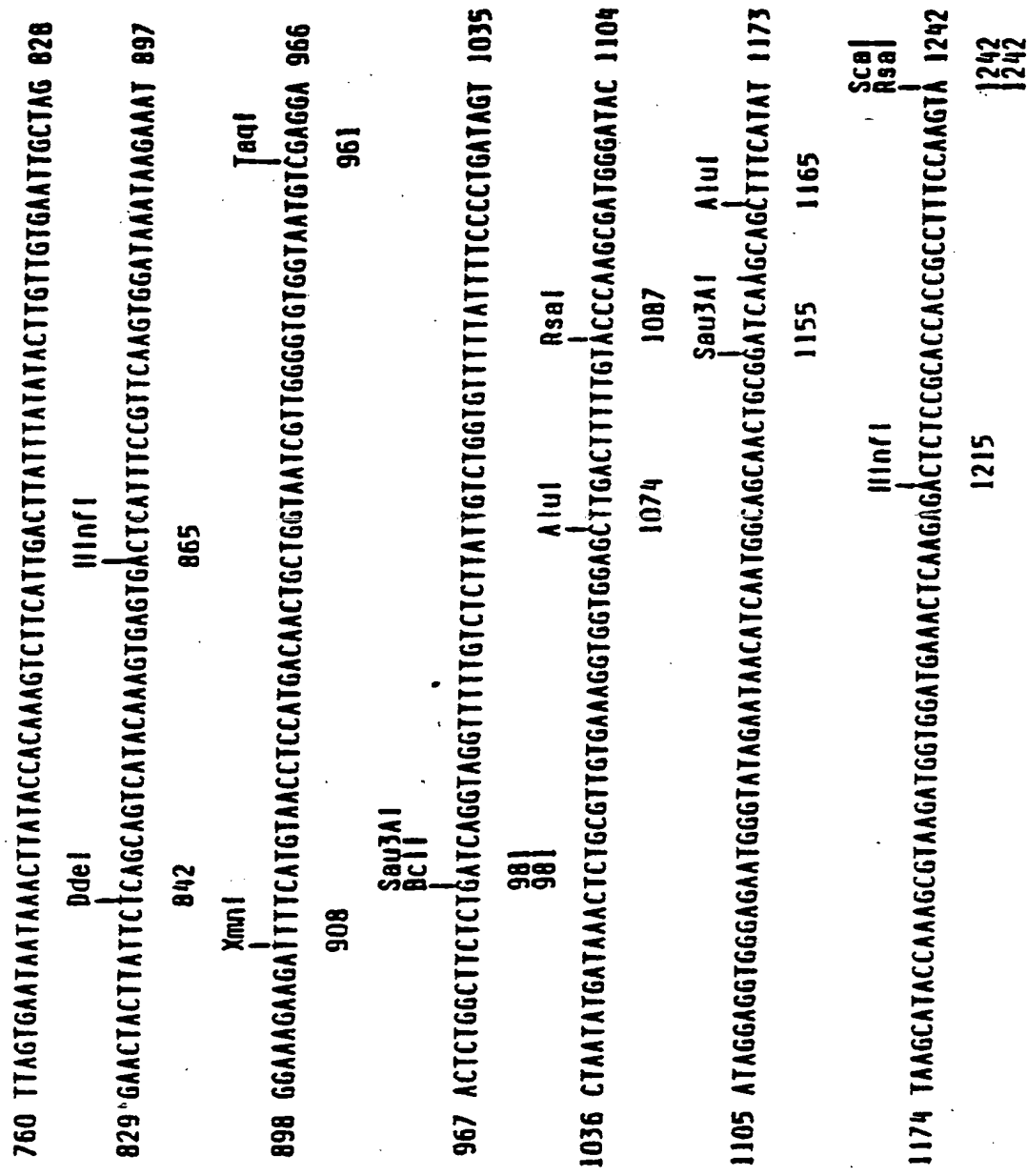


FIG. 2C

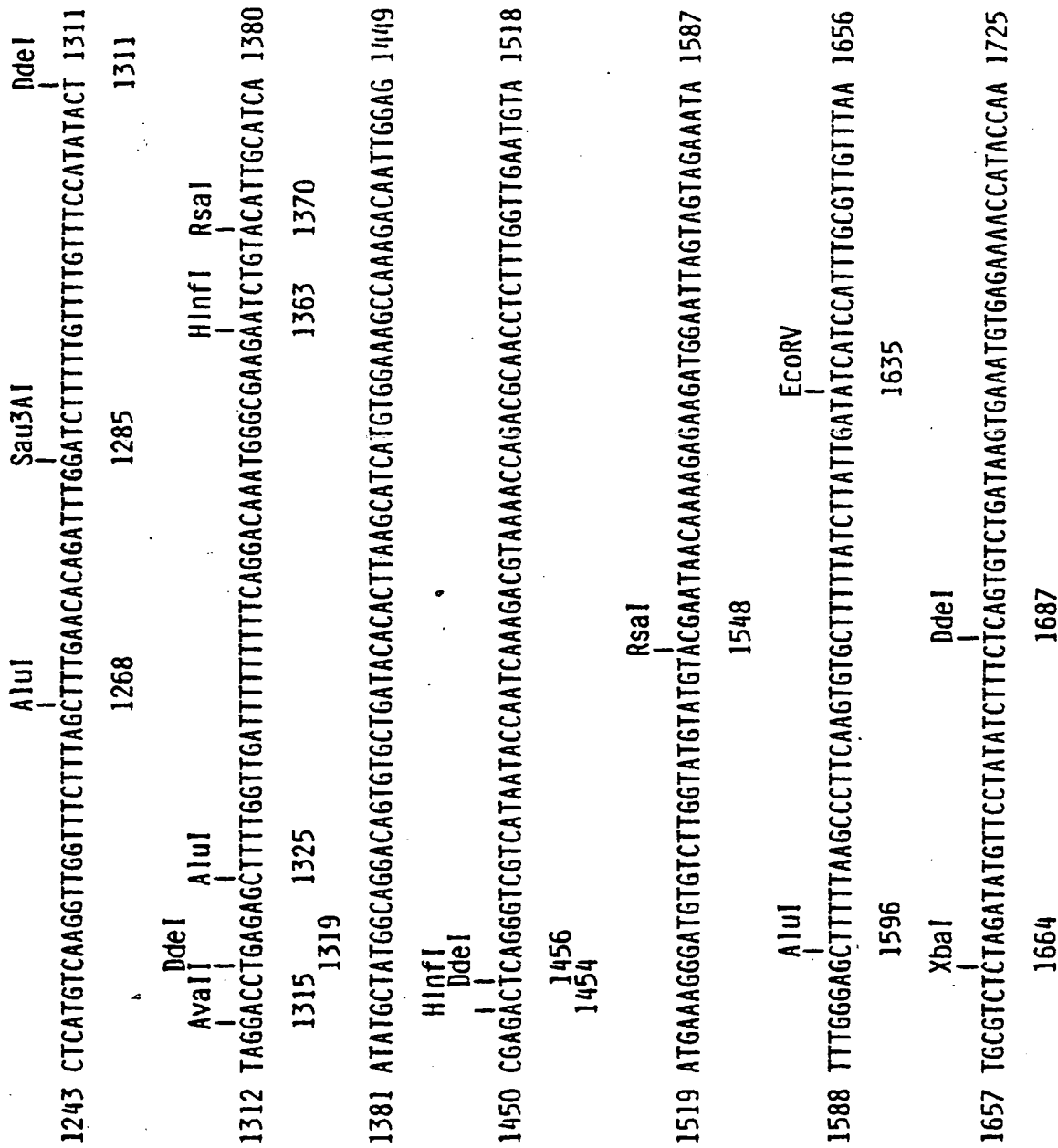


FIG. 2D

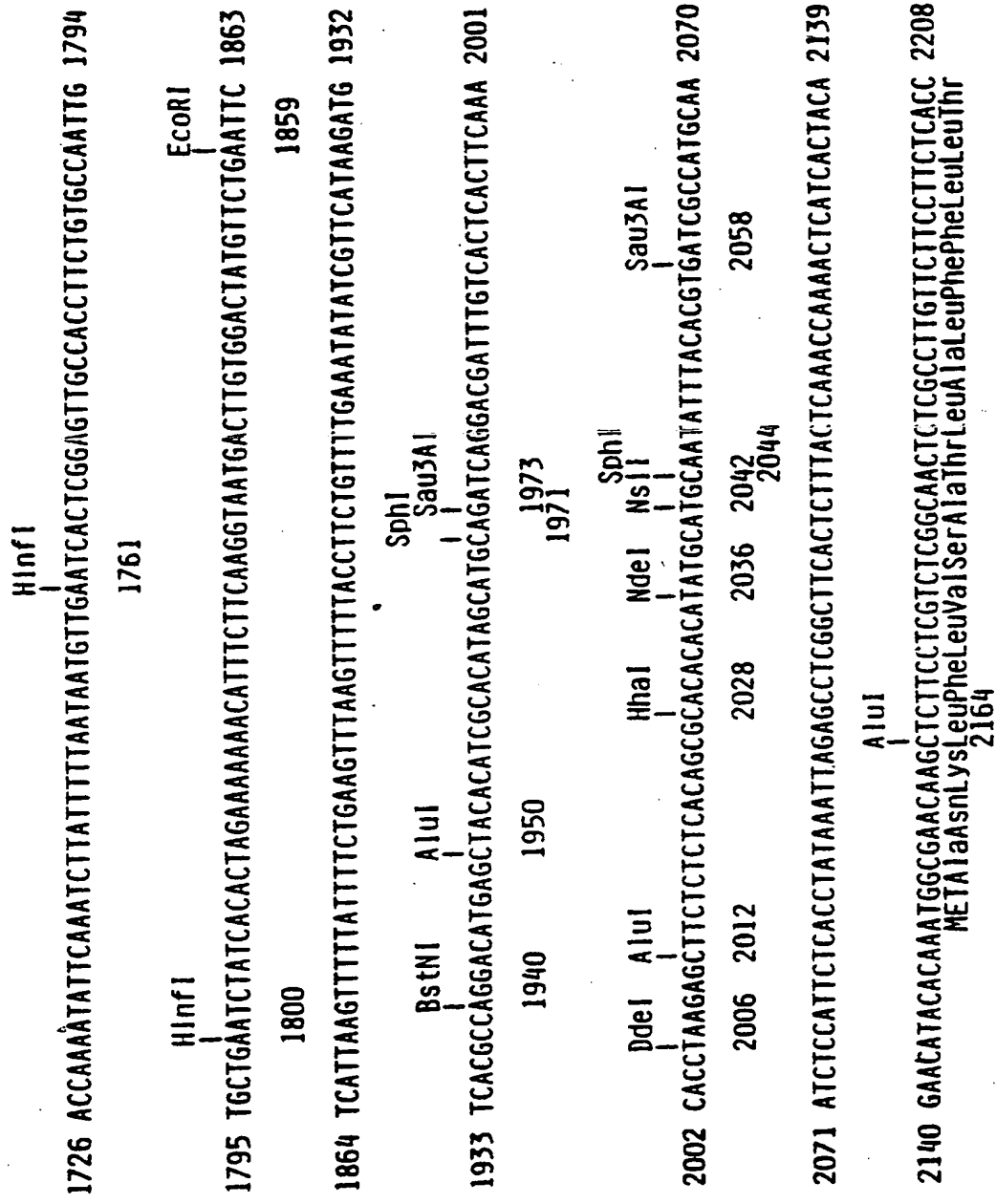


FIG. 2E

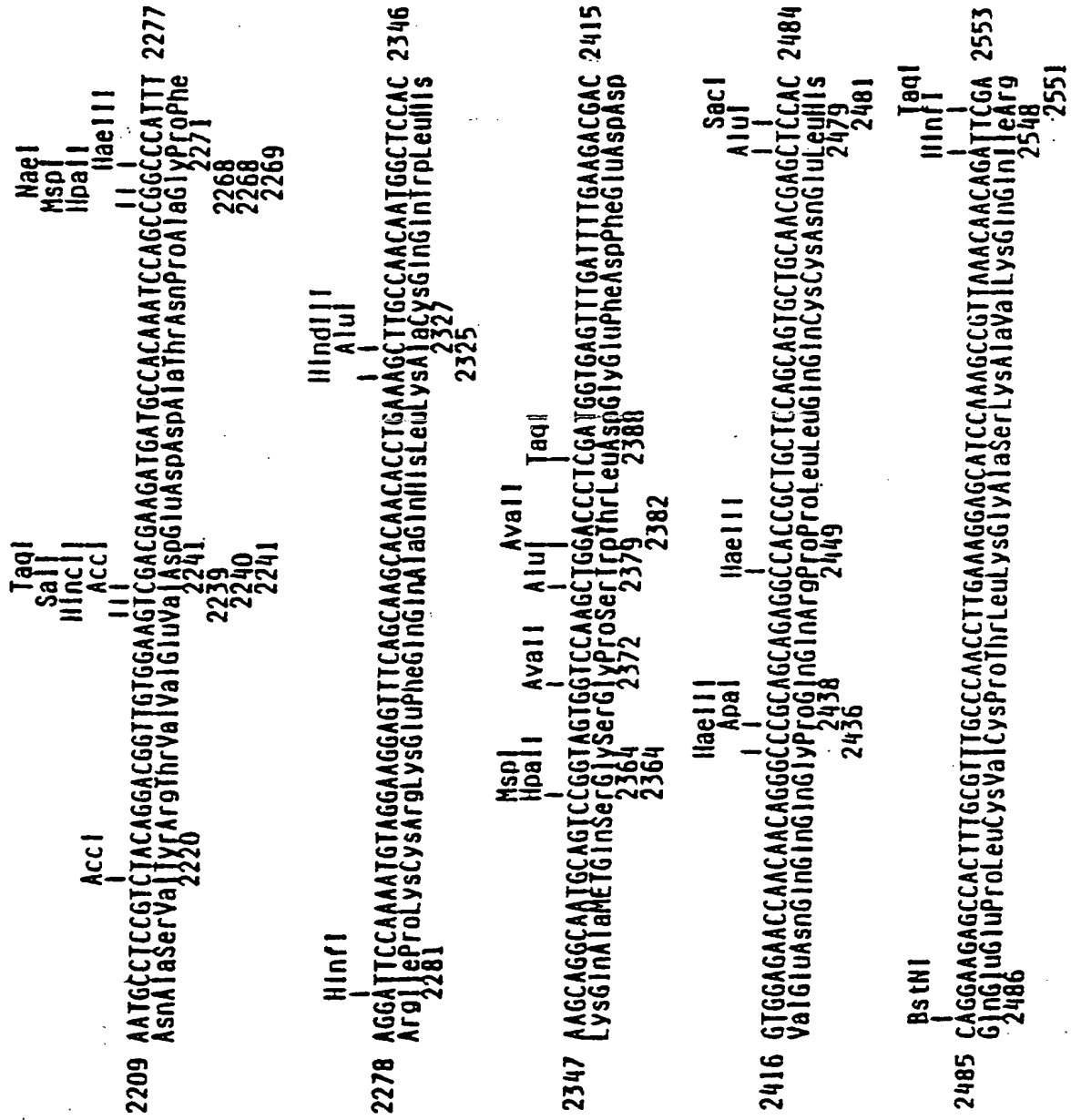


FIG. 2F

FIG. 2G

2968 CATGTCAGATTTTCTTTTCTAAATGCTAATTAAGCCTTCAAGGCTAGTGATGATAAAAGATCATCCA 3036
 Sau3AI
 3028
 3037 ATGGGATCCCAACAAGAGACTCAATCTGGTTTGGATCAGATACTTCAAAACTATTTTGGTATTCATTAAA 3105
 Sau3AI
 HinfI
 3041 3053 3069 3069
 3041
 3016 TTATGCAAGTGTTCTTTTATTTTGGTGAAGACTCTTTAGAGCAAGCAAGCAGTAATAAAAAA 3174
 HinfI
 3135
 3175 ACAAGTTCAGTTTAAAGATTGTTATTGACTTATTGTCTATTGAAAAATATAGTATGATATTATATA 3243
 3244 GTTTTATTATATGCTTGTCTATTCAGATTGAGAACATTATATGATACGTCCACATATCCA 3312
 NdeI
 3313 TATATTAAGTTTCATTTCTGTTCAACATATGATAAGATGGTCAATGATTATGAGTTTGGTATTAC 3381
 3341
 3382 CTGAAGAAAGATAAGGAGCTTCGAGTTTCTGAAGGGTACGTGATCTTCATTCTTGGCTAAAGCGA 3450
 AclI
 TspI
 Sau3AI
 RsaI
 3402 3421 3405 3425
 3451 ATATGACATCACCTAGAGAAAGCGGATATAGTAAAGCTGTTCTGGTTTTGGTTTATCAACCGA 3519

FIG. 2H

MspI DdeI
 PstI Aul
 3522 3528
 3522 3529
 3520 ACCGGTAGCTGAGTGTCAAGTCAGCAACATCGCAACCATAATGTCAAATCGTTAGATCCCGGTAA 3588
 MspI
 PstI
 HinfI
 NdeI
 3576 3581
 3576 3581

Hsp
 11pa |
 3589 GTTGTAACCGGTATTTTCATTTGGTGAAACCCCTAGAACCCAGCCANCCYTTTTAAATCTAATTTTGGCA 3657
 3598
 3598

3658 AACGAGAGTCCACCACCTCTCTCCACTAAACCCCTGAACCTTACTGAGAGAGAGCAGAGNCANHAAGA 3726

3727 CAAATAAACCCGAAGATGAGACCACCACTGC GCGGGACGTTCA GGGGACGGGGAGGAGAATGR 3795

AvB || | | |
| | | | |
AvB || | | |
| | | | |

3796 CGGCGGSMNTT TGGTGCGCGCGGACGTTTTGGTGCGCGGTGGACGTTTTGGTGGCGCGGTGGG 3864

Avall
3804
3801 3863

3865 CCYTTGGTGGGATACGTGACGAAGGACCCTCCAGTGAAGTCATTGGTTCGTTACTCTTTCTAG 3933

ECORV AclI DdeI

3880 3892 3930

FIG. 21

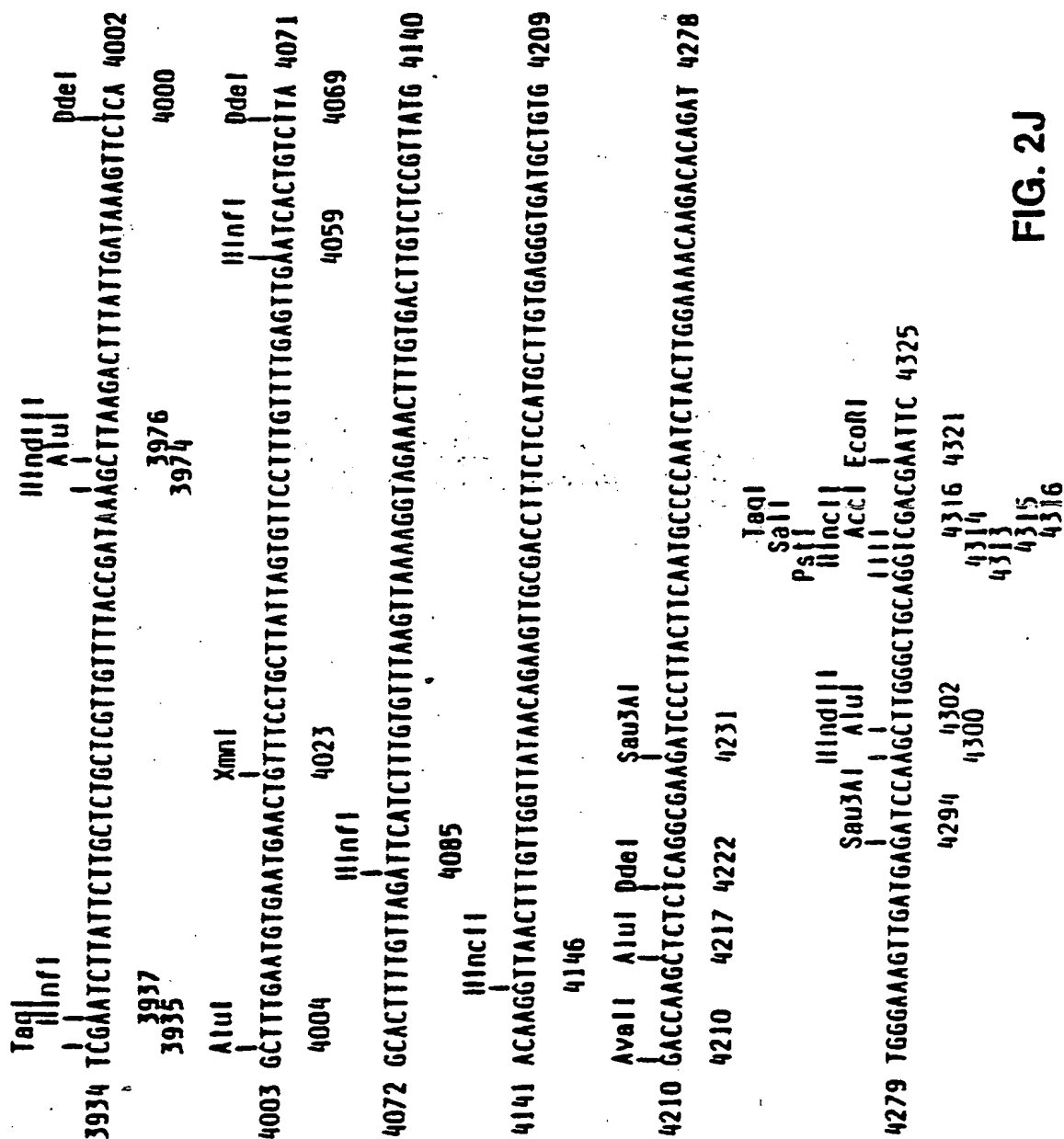


FIG. 2J

Brassica campestris ACP Genomic Sequence

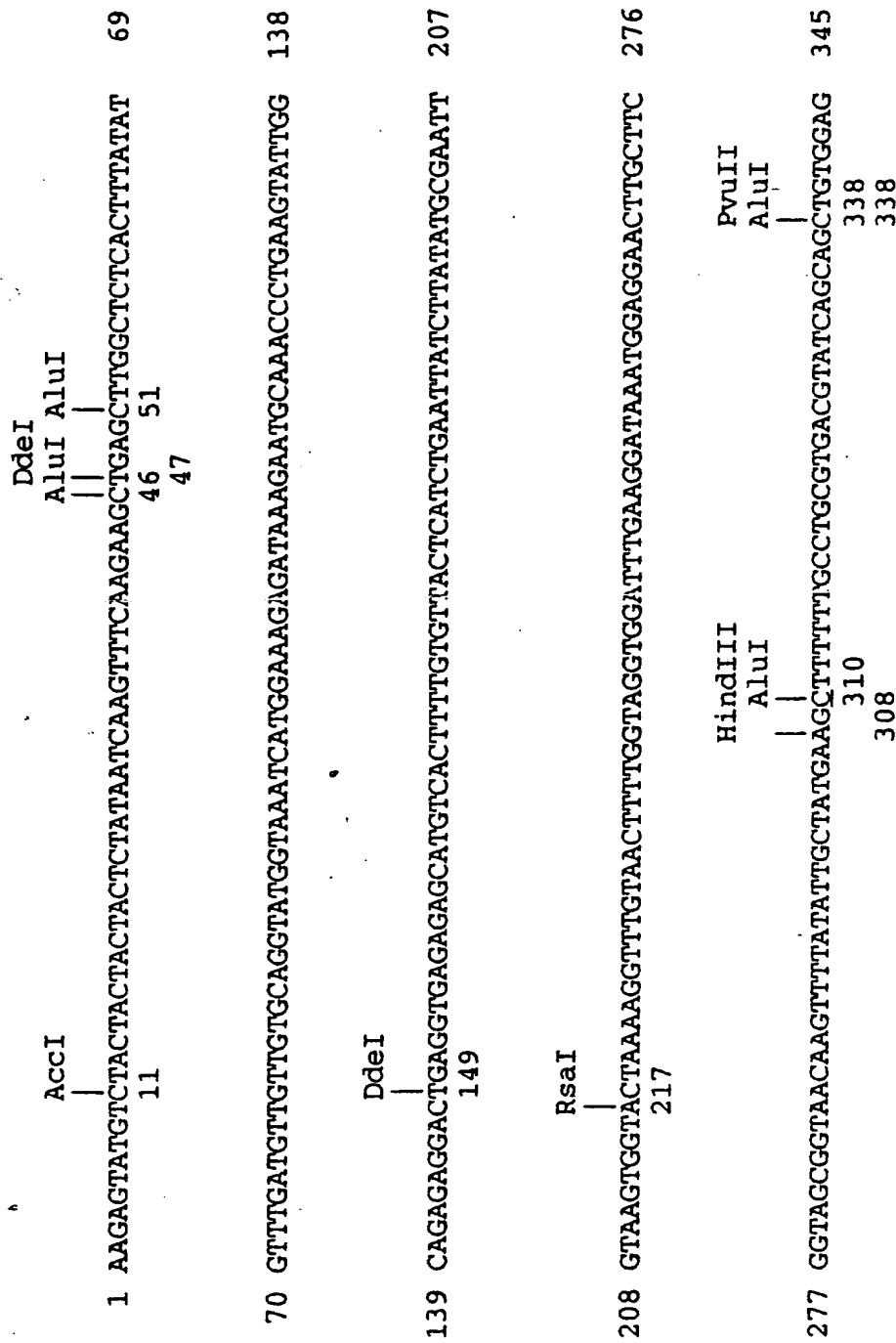


FIG. 3A

GENE

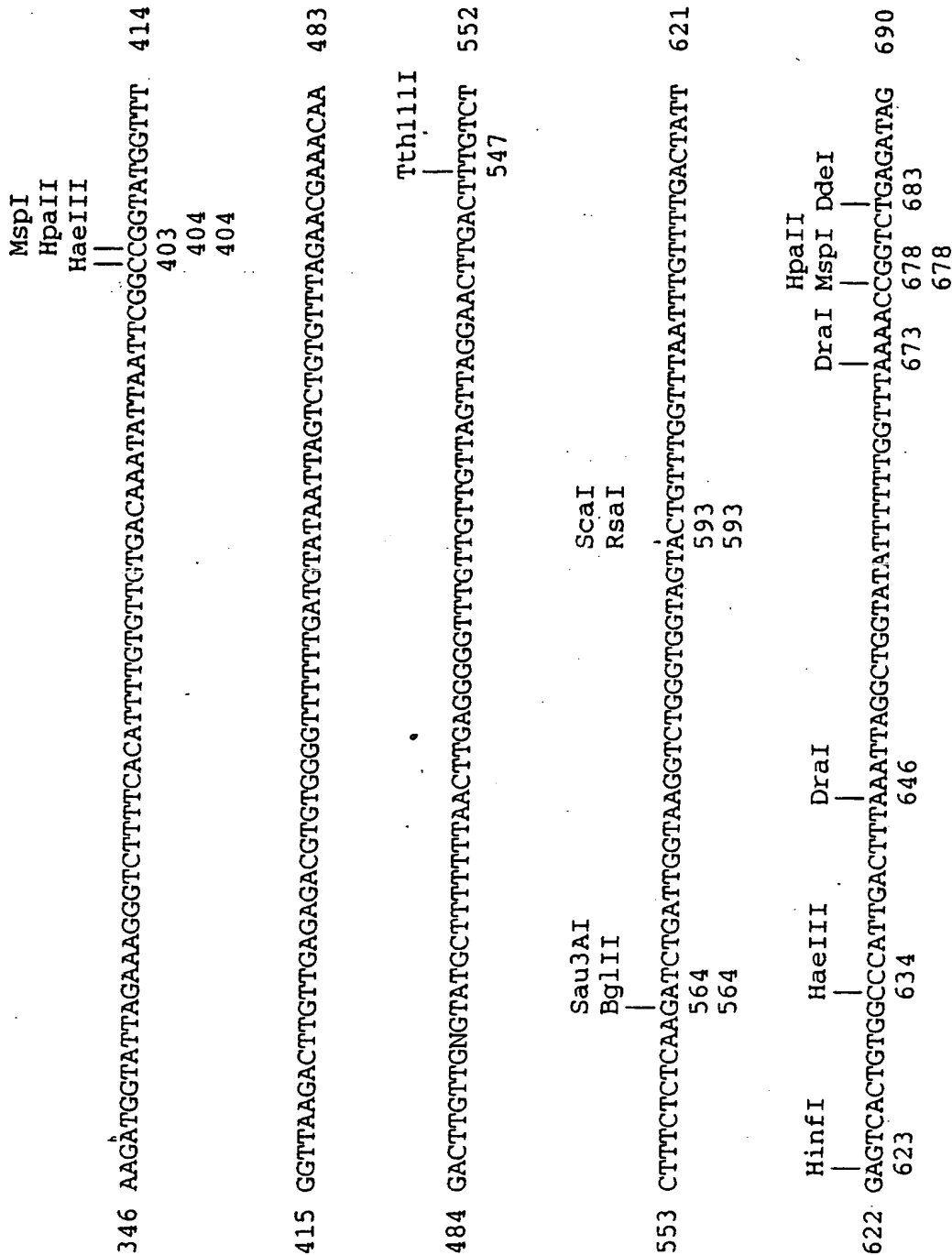


FIG. 3B

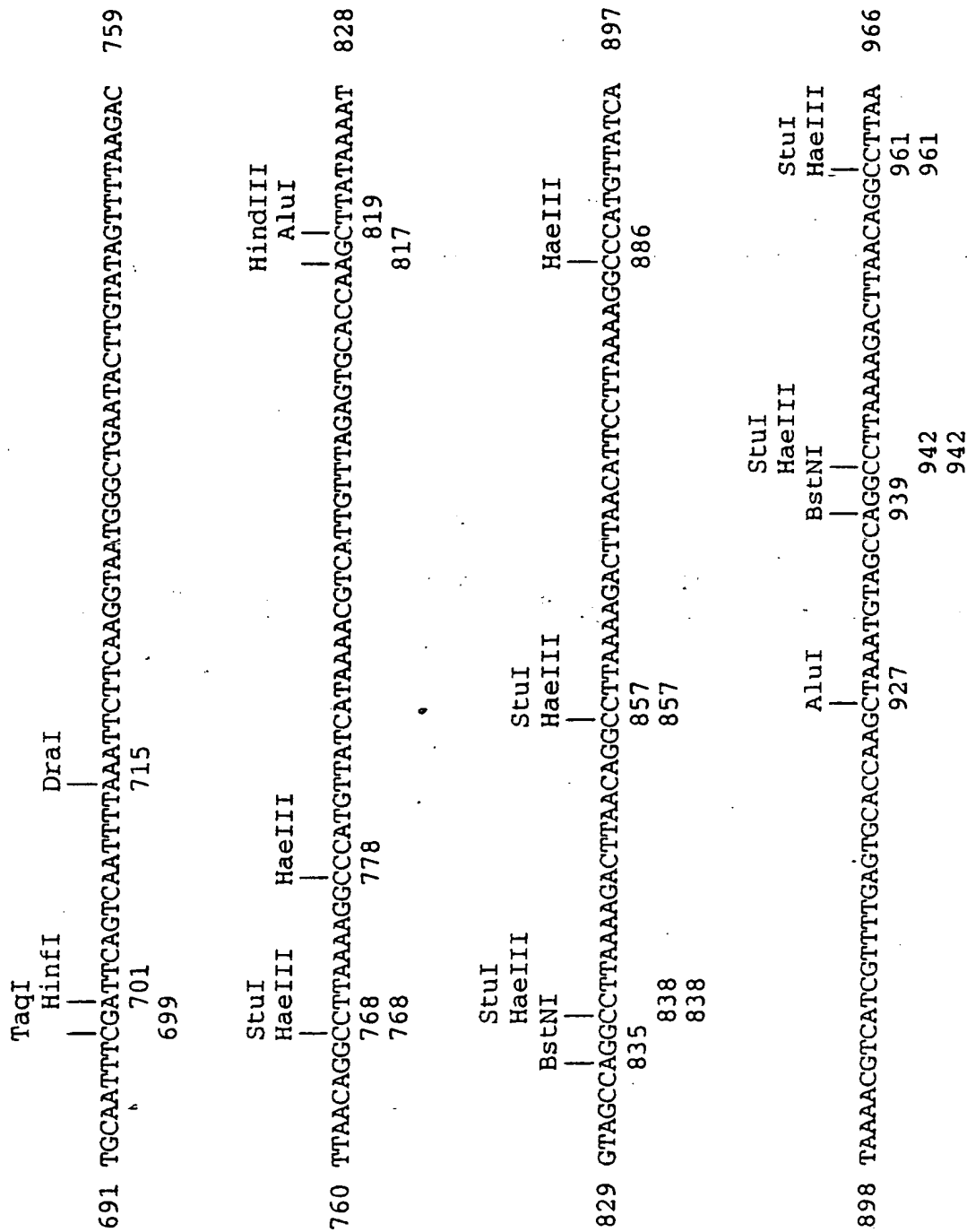


FIG. 3C

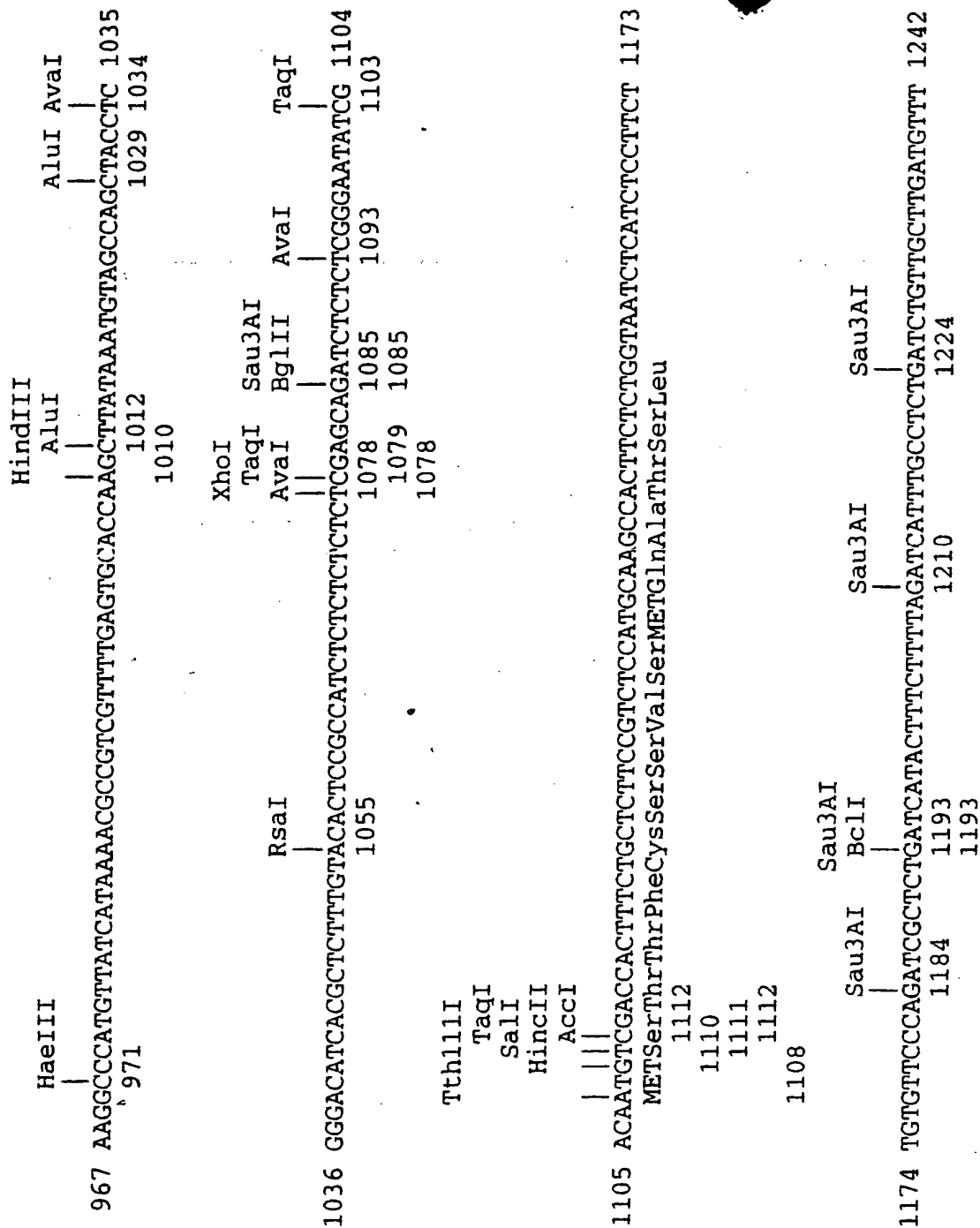


FIG. 3D

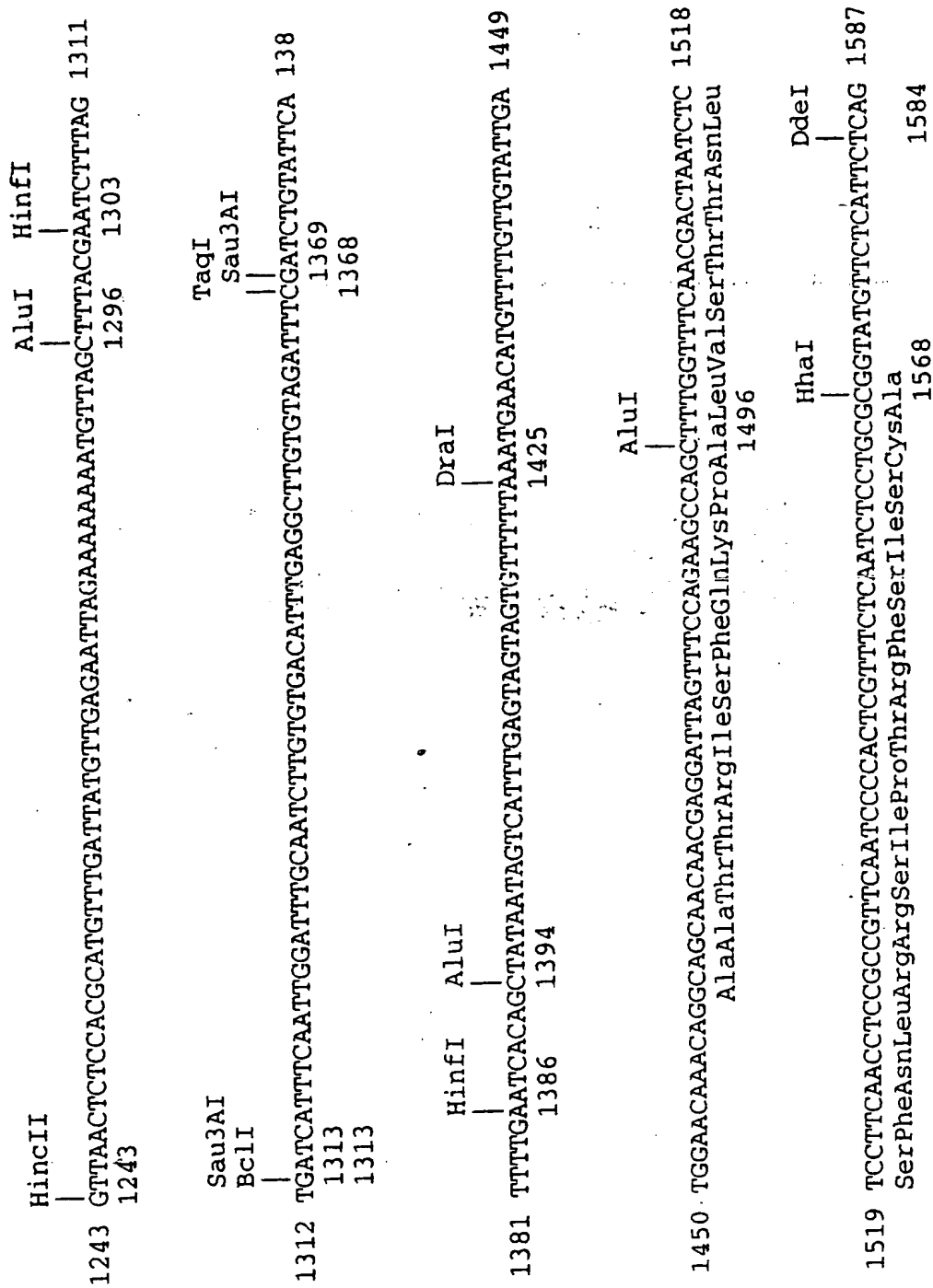


FIG. 3E

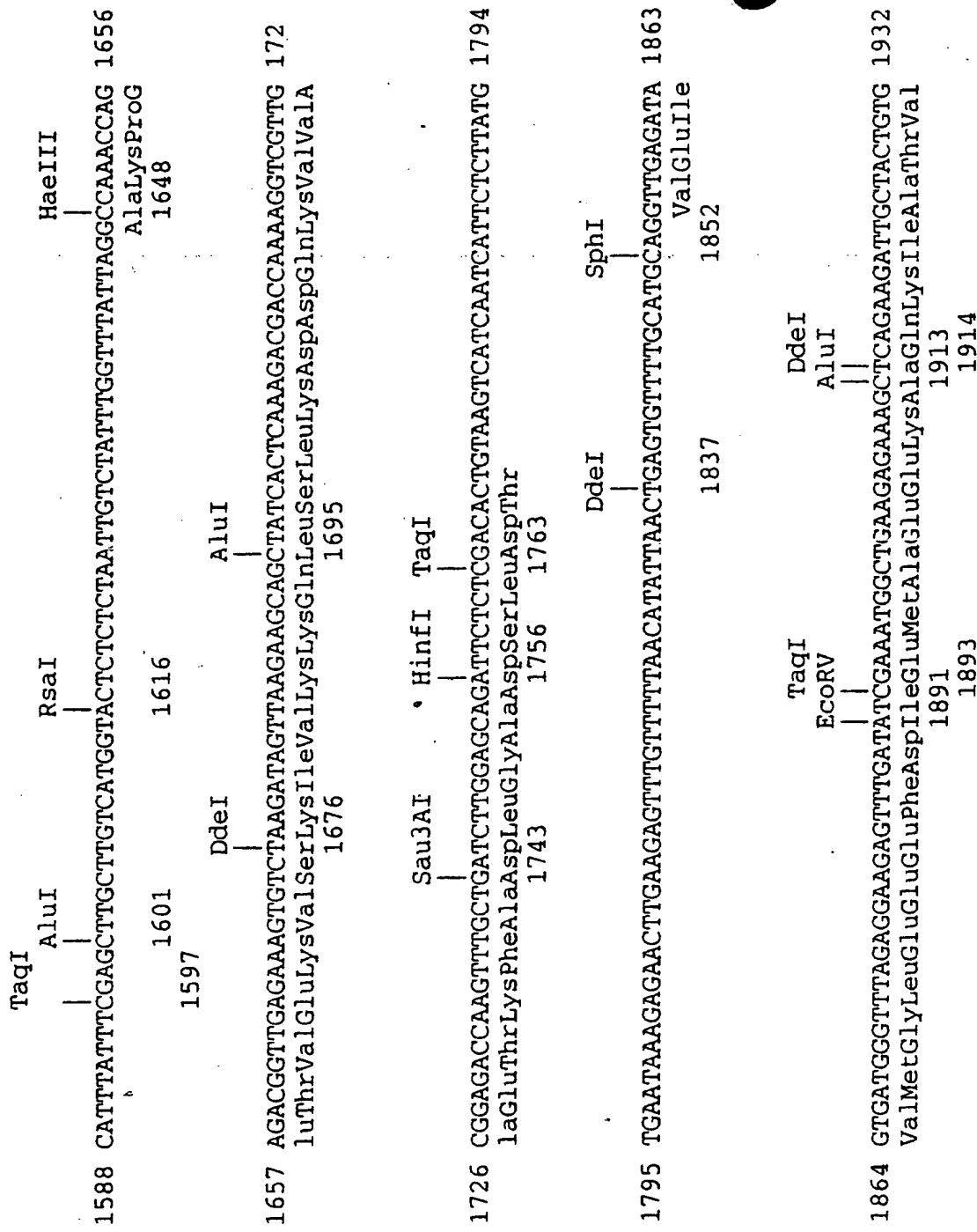


FIG. 3F

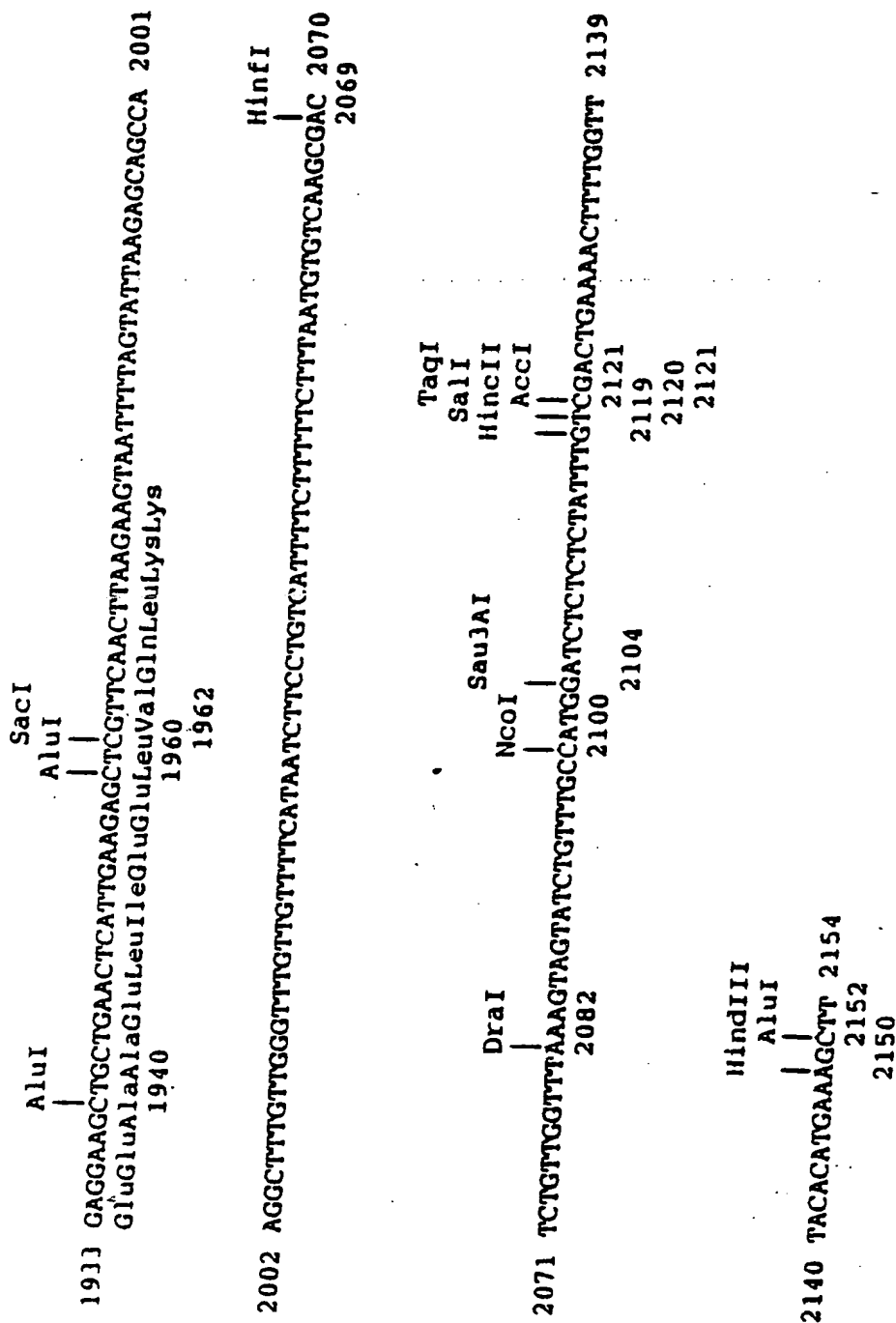
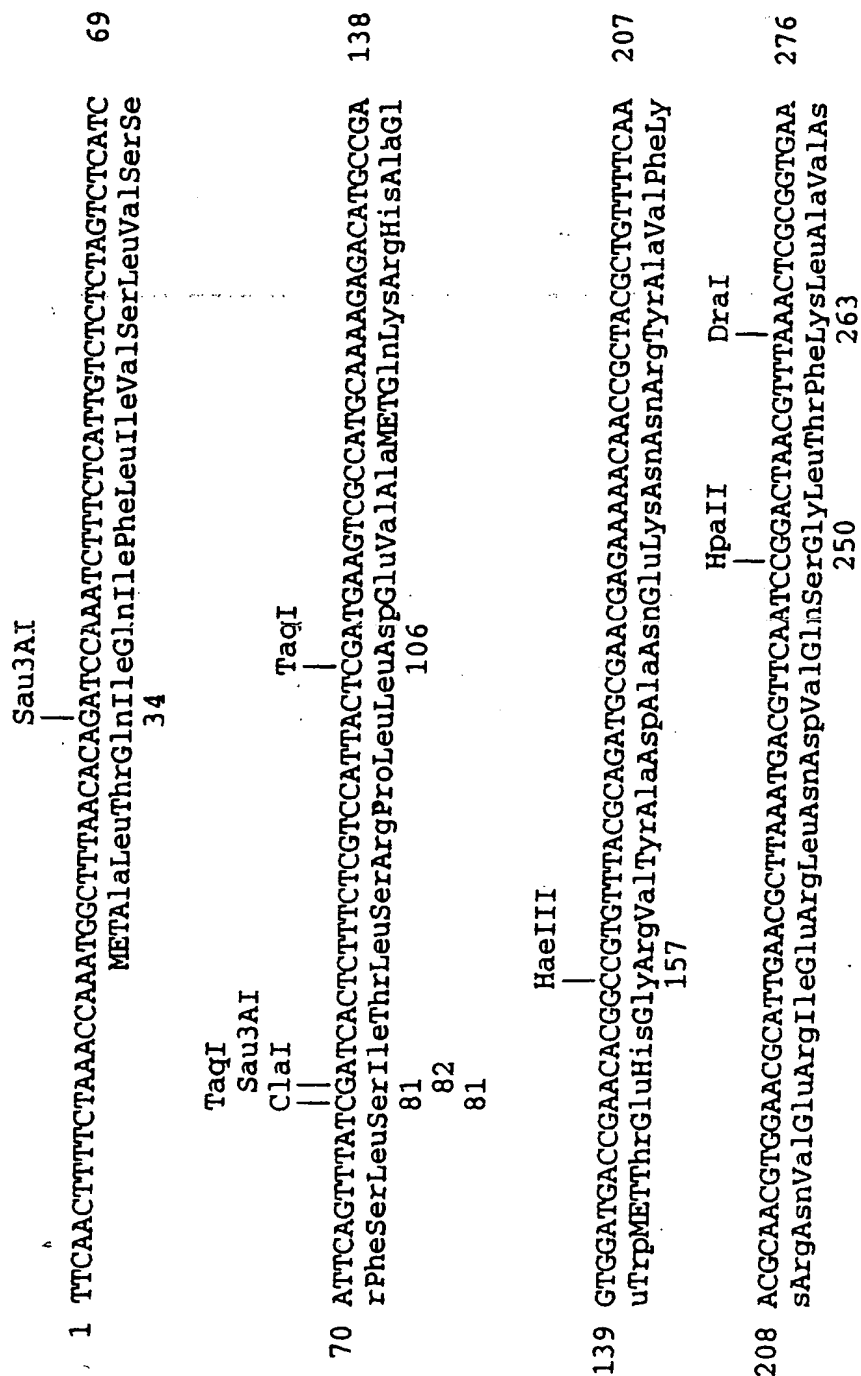


FIG. 3G

Brassica Campestris Seed Specific cDNA-EA9



Complete nucleotide sequence of *B. campestris* cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of the sequence and a potential polyadenylation signal is underlined.

FIG. 4A

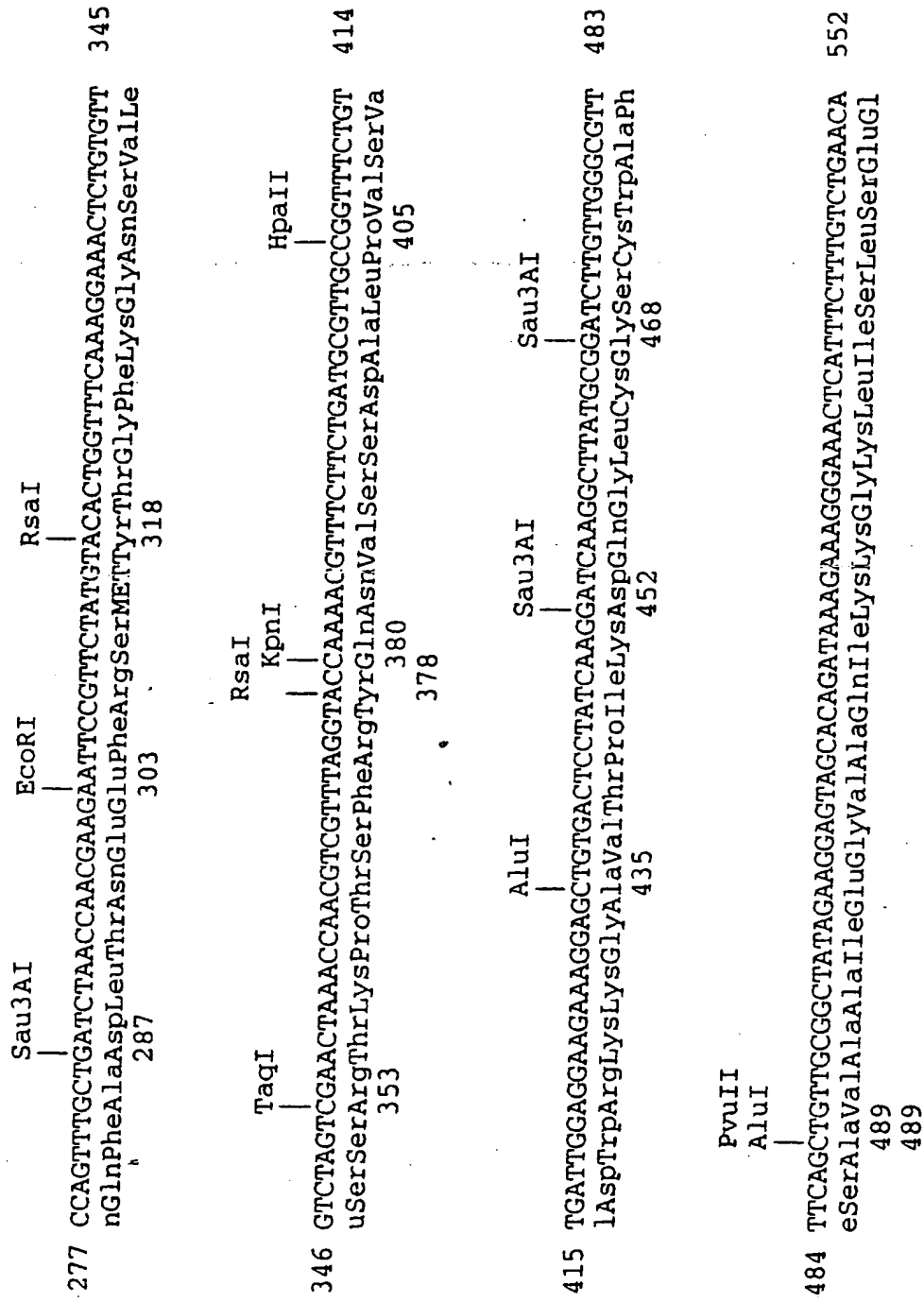


FIG. 4B

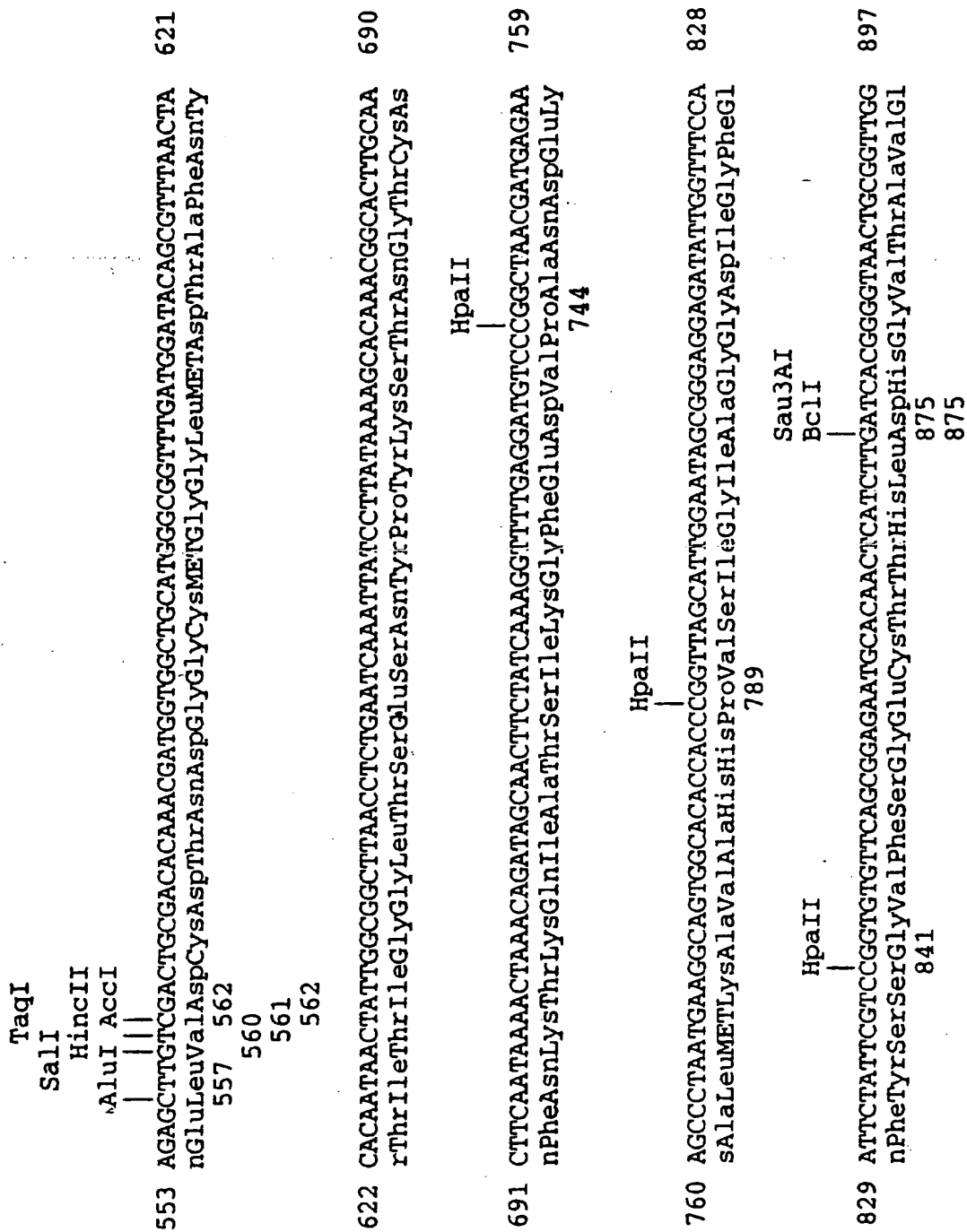


FIG. 4C

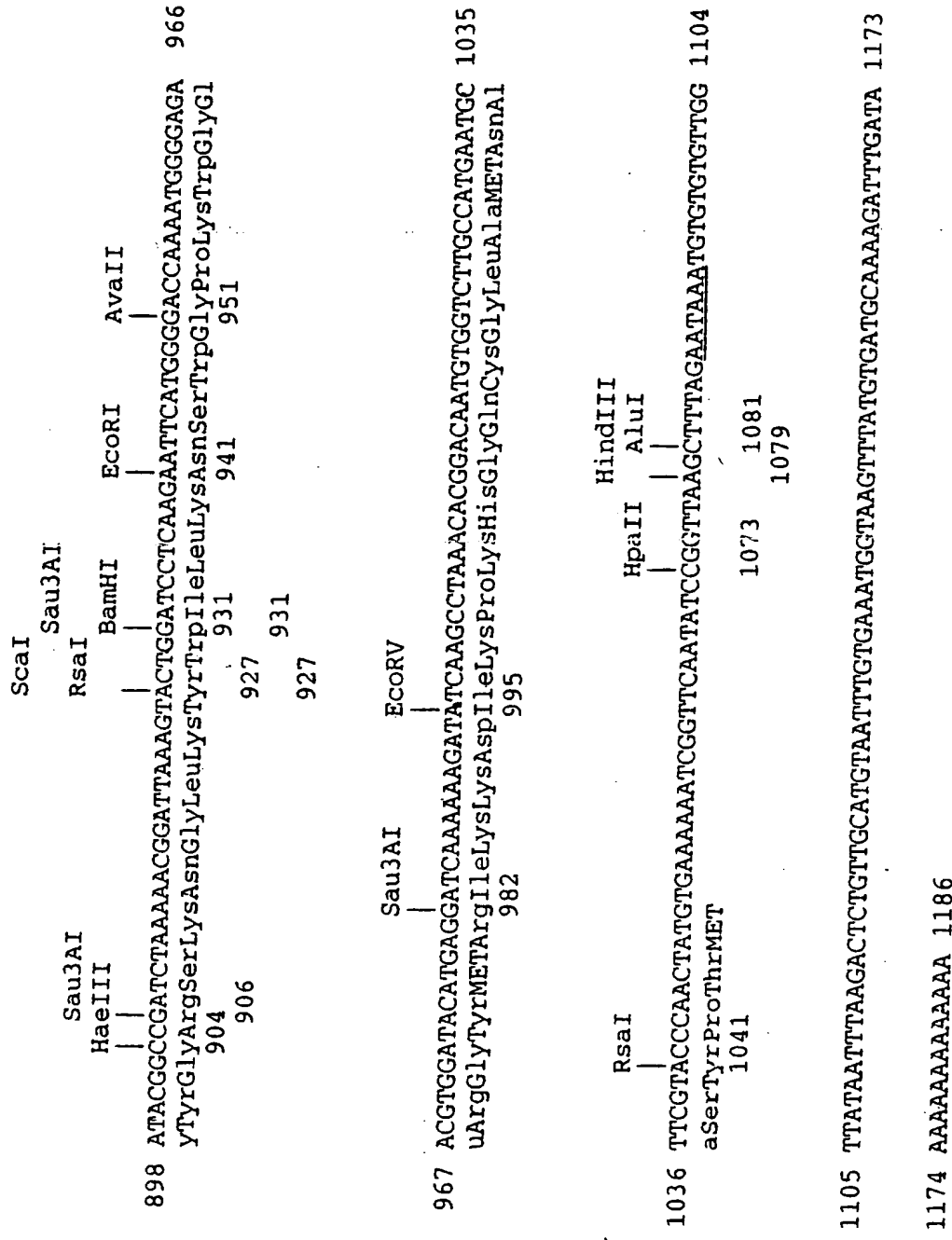


FIG. 4D

3H11 TTTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA 51

3H11 GCTTACAGCTGGGAGAACATTGTCTAACTCTTCTGAAATTTAAATGTTATC 102

3H11 CAGAATCCTTCATCATAAAATAATATCAAAATGCAAATCTATTTTTTCTAC 153

3H11 TCTTGTCTAGCTTCAACTTTCTTCTTCTGCTCATCAATTAGCAATTAATCC 204
TGCTCATCAATTAGCAATTAATCC

3H11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC 255
2A11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC
METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe

3H11 GTTGTTCCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTGAAAATG 306
2A11 GTTGTTCCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTGAAAATG
ValValLeuLeuThrThrThrLeuValAspMETSerGlyIleSerLysMET

3H11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG 357
2A11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG
GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET

3H11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA 408
2A11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA
LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer

3H11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG 459
2A11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG
AsnSerAspCysIleGlyIleThrLeuCysGlnPheCysLysGluLysThr

3H11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCTTGAACAATA 510
2A11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCTTGAACAATA
AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro .

FIGURE 5A

3H11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA 561
2A11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA

3H11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612
2A11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT

3H11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT 663
2A11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT

3H11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATTCCACATTAAT 714
2A11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATTCC

3H11 TCACGTATTTATTTCACTTATGATACGTATTTTTGTTCCTTTCGCGTAAAA 765

3H11 AAAAAAAAAA 774

FIGURE 5B

2A11	①MALRDIPPQETLL
PA1b	①CSPFDIPPCGSPLCRCI
Chick pea inhibitor	①CT-KSIPP-----QCRCN
Lima bean inhibitor	LCT-KSIPP-----QCRCT
α_1 -antitrypsin	LGAIPMSIPPEV

2A11	TNILLGLCNEPCSSNSDCI
PA1b	GSPLCRCPAGLVIGNCR
Barley chloroform/ methanol-soluble protein d	TNLLGNCR-FYLVQQTCA
Wheat α -amylase inhibitor 0.28	VSALTGCR-AMVKLQ CV
Wheat albumin	VPALPACRPL-LRLQ-CN
Millet bi-functional inhibitor	NNPLDSCRWYVS _A TR-TCG
Castor bean 2S small subunit	QQNLRQCQEYIKQQVSGQ
Napin small subunit	AQNLRACQQWLNKQAMQS

FIGURE 6

2A11 GENOMIC

10	20	30	40	50
CTCGAGCCCT	TTAAAAAGTA	TAGTCAATAT	TTACGGTGAC	CGTGAATTTT
60	70	80	90	100
TTAATTATGA	TATATAATTT	AAAAGAAATC	ATGATCACAT	TCTACTGATG
110	120	130	140	150
AGAACATGTG	CTAATCAAGG	GAAAACATGG	ATGTGAAAAA	TACTTTTTGT
160	170	180	190	200
TAAAAGTAAA	AAAAAATGTG	AAATTTTGTT	AGTTATTTAC	TACCTATACA
210	220	230	240	250
TTATTTGAGC	ATGTGCAAAC	TTTACAAATA	CCTAATAGAA	GATTTTCACC
260	270	280	290	300
TGCCTGTATA	TATGTAAATT	AATTATAATG	AACACTCTCA	CATAAAATAA
310	320	330	340	350
TTATCAGTAT	ATACATTAAT	ACTTGCCCTC	CACAATGAAT	TAAATAAAAT
360	370	380	390	400
GTAGAACATG	ATCTACACTT	CAATAAAACT	AAGACCATAA	AGAATAATTT
410	420	430	440	450
CAAAATATAC	ACATGTCAAC	AATAAATTAT	TTGCATATTA	TATTAECTTA
460	470	480	490	500
CTAAACAATC	TTTACTTTTG	AAATATAAAA	ATAATCAAGT	TATAAGTCTG
510	520	530	540	550
CTCAAAGTAA	AGCACTTGTT	AGACTCATCT	GATTTTGAGA	AGGTAAGCAA
560	570	580	590	600
ATTGATGGTG	CATAATAGTC	ACAAGTAAAA	TATAAAATAG	ATTTTCATTAG
610	620	630	640	650
TAAAATTGTT	TTTTACTTTC	TTTATATATA	ATTATCAATA	TCCTTCAATG
660	670	680	690	700
GTAGGTTAAT	TATATTGTTA	ACTTCTTGTT	GAATTAAAGC	AATAAGACAA
710	720	730	740	750
GAATATTAAA	GATAAAAGAA	CAATAAAAAT	AGAAAGACTA	AGAGATAAGA
760	770	780	790	800
GTTTTCTTAT	TCTTCTTTCA	ATAAGTATCA	TCAAGTGTAT	ACAATATAAA
810	820	830	840	850
TTTTTGTATT	TTTGATCTAT	CTATTTATAA	TGTTATATAT	AAGCATACAA
860	870	880	890	900
AAGATCAGTC	ATAAATATGA	CTTTAATCAT	GAAAATAATG	AAAGAGATTA
910	920	930	940	950
TGAAGGCGTA	AGGTTACTAG	AATAATAGTC	ATTAAAAAAA	GGGGTTATCT
960	970	980	990	1000
TTATAATTGA	ATAATTGATG	AAGTAATGGA	GATAATTAGT	GAGCATAAAT
1010	1020	1030	1040	1050
TTTTTTAAAA	AAATGGACAT	TTACACTATA	ATATTTTATA	ACACTTTCCC
1060	1070	1080	1090	1100
TTAAACATCT	AGGTATAAAT	AATGAGTCTT	GTCAAAATCT	TAGTAGGAAA

FIGURE 7A

1110	1120	1130	1140	1150
AATTCTGTGA	AATTTTTTTTA	GTGAAAACAA	ATGATATAAA	TATCTTGAAT
1160	1170	1180	1190	1200
ACTCATTATT	TGTTGTCTCA	TTAAAAATCT	TATCTGACCT	ATAAAATAAA
1210	1220	1230	1240	1250
TTATTTGCTC	AACTCAAAAT	AGTTTTTCAT	TCTAAAATTA	GTATAATTAT
1260	1270	1280	1290	1300
TAGTGAATAT	TTAATTAACA	TAATTGTATA	CTAAGGGGCC	TATAAATTGG
1310	1320	1330	1340	1350
ATTCTTCTCA	AAGAAAAATA	AAATCACCAC	ACAACCTTCT	TCTTCTGCTC
1360	1370	1381	1390	
ATCAATTAGC	AATTAATCCA	AAACCATT	ATG GCT GCC AAA AAT	
			MET Ala Ala Lys Asn	
1399	1408	1417	1426	
TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT GTT CTT TTG				
Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val Leu Leu				
1435	1444	1454	1464	1474
ACG ACC ACT TTA GGTTCACAAC	ACTTCTCCCT	TATTTTGTTT		
Thr Thr Thr Leu				
1484	1494	1504	1514	1524
TCTTAATTC	TTGGAAGTCA	TATGCATGTG	TTTGGTATCA	TGGTATATAT
1534	1544	1554	1564	1574
ATAAAGGAAA	ATATTTTCT	TAATTACTGG	TTTTCTAATG	TTTGGTAGGT
1584	1594	1604	1614	1624
AATCGGAAAT	TATTATGAGA	TAATGAACCT	GCAAAGTCAT	TATTATATAA
1634	1644	1654	1664	1674
CTTTTTTTT	ATACTTTGAT	TTAAGAATTC	ATTTTTCTCA	TTTTATATAA
1684	1694	1704	1714	1724
ACTTATTTT	CAACAGAAAA	TATTTTTTCGA	ACTATTCAAA	CACACCCTAA
1734	1744	1754	1764	1774
GACATTACAT	ATATATATAT	ATACACCCTC	CGTTTTATAT	TACTTAATGC
1784	1794	1804	1814	1824
CTATTGAGTT	GGCCCACCCT	TTAAGAATGA	TTCAATTAGA	GATATGTTTT
1834	1844	1854	1864	1874
ACTAAATTAA	CCTATGCTTT	AAGACTCTAA	ATTTGGCTAT	TACTATTTTA
1884	1894	1904	1914	1924
CGTTGTAATT	TAATGACAAA	CATTTCAATA	TGACTATAGT	CTGAACTTAA
1934	1944	1954	1964	1974
TTAGACAGAC	GTATCTATAG	TTTGCTTACT	AATGATTCAT	AGCTATATAT
1984	1994	2004	2014	2024
TTGGAGAGGA	GAGAGACAAA	CGATATTAAG	AAAGGGAGGA	GAGAGGCGAG
2034	2044	2054	2064	2074
GTAAATCTGA	AATAGAGAAG	AGAAAGGCAA	CCAATTTTGA	TCATCTATCA
2084	2094	2104	2114	2124
TACTTTTGAT	TATTATTTTT	ATTATATGTA	CGTTTACATT	ACAGTTTTTCG

FIGURE 7B

2134	2144	2154	2164
AATTCTTACA	TTAATCTTAA	TCATAATATA	TACA GTT GAT ATG
			Val Asp MET
2173	2182	2191	2200
TCT GGA ATT	TCG AAA ATG	CAA GTG ATG	GCT CTT CGA GAC
Ser Gly Ile	Ser Lys MET	Gln Val MET	Ala Leu Arg Asp
2209	2218	2227	2236
ATA CCC CCA	CAA GAA ACA	TTG CTG AAA	ATG AAG CTA CTT
Ile Pro Pro	Gln Glu Thr	Leu Leu Lys	MET Lys Leu Leu
2254	2263	2272	2281
CCC ACA AAT	ATT TTG GGA	CTT TGT AAC	GAA CTT TGC AGC
Pro Thr Asn	Ile Leu Gly	Leu Cys Asn	Glu Pro Cys Ser
2290	2299	2308	2317
TCA AAC TCT	GAT TGC ATC	GGA ATT ACC	CTT TGC CAA TTT
Ser Asn Ser	Asp Cys Ile	Gly Ile Thr	Leu Cys Gln Phe
2326	2335	2344	2353
TGT AAG GAG	AAG ACG GAC	CAG TAT GGT	TTA ACA TAC CGT
Cys Lys Glu	Lys Thr Asp	Gln Tyr Gly	Leu Thr Tyr Arg
2371	2380	2393	2403
ACA TGC AAC	CTG TTG CCT	TGA ACAATATCAA	TGATCTATCG
Thr Cys Asn	Leu Leu Pro		
2413	2423	2433	2443
ATCGATCTAT	CTATCTATTT	ATCTGTCTCT	GCGCGTATAG
2463	2473	2483	2493
ACCTTTGGTG	TGAAGAATAT	GAATAAAGGG	ATACATATAT
2513	2523	2533	2543
TCTAGGTAAT	GTCCTATTGT	ATTTAAAATT	TGTAGCAATG
2563	2573	2583	2593
TAAAAACATA	CCATGAGTGA	AATAATTATT	CCACATTAAT
2613	2623	2633	2643
ATTTCACTTA	TGATACGTAT	TTTTGTTCCT	TTCGCGTAGA
2663	2673	2683	2693
TTTTCCCTTT	TGAATATTAA	ACATTAAACA	CAAATAATGT
2713	2723	2733	2743
AAGTTAATAT	TTTTATTTAG	CTATTTATAT	TTTTATTTGA
2763	2773	2783	2793
GATAAATATT	TATAAAGATA	ATTAACAAGT	AATGTGACAC
2813	2823	2833	2843
TAATATTATC	TTGTCGTTAT	TTATGATAAT	ATTTTAAAAT
2863	2873	2883	2893
GTTAAAAAAT	TATTAAAAAA	ACATACTTTT	AAAAAGTGAG
2913	2923	2933	2943
CTACCCACAT	ACTTATGAAT	TGGACTAGTT	GTTTTTTGAC
2963	2973	2983	2993
AATGGGGCTAA	TTAAACCTGA	CCTATCAAAT	TTCAGAATCT
			GCATAGATTA

FIGURE 7C

3013	3023	3033	3043	3053
GTCCGAACGA	AATGAGTCAG	CCCGTATTGA	ACAAAATATC	AACAAGGACG
3063	3073	3083	3093	3103
TTATGTAAAG	ATGTTTAAGA	AGGAAAAAAG	ATTTCTAATA	CATATGGACT
3113	3123	3133	3143	3153
TTCAATATCC	CAACTTTGTC	TGGCGATCTG	AACCCTGCTT	AGTTTGTGTA
3163	3173	3183	3193	3203
TCATTAACCT	GTCTTGCTAT	GTATTTAAGA	TTTAAACTTT	ATATGTTTAA
3213	3223	3233	3243	3253
ACTTACAGAA	AATACATATA	AATCTCTCAA	GACTTGGCAA	CATAATTTAC
3263	3273	3283	3293	3303
TTTAGTACTT	AACTACATG	AAAATTTTAA	TATCCTTTTA	ACATCTTTGA
3313	3323	3333	3343	3353
AGTGAATTAA	ATTATCACAA	TCCGAGCCTA	CACCTTGGAC	GTGGCCCGCA
3363	3373	3383	3393	3403
CTCAAGAACC	AGTGCTGGTC	CCCAAGCTAA	CCCTCATCCT	GACTGACTAC
3413	3423	3433	3443	3453
AAGCGGAAGG	CTAACTTAAG	TATACAAAAG	CTTAAACTTG	AATAAAATAA
3463	3473	3483	3493	3503
ACTTTACAAG	GTTTTAACAC	AAATGAACAA	CTTTGAAGAA	AATAATATAT
3513	3523	3533	3543	3553
TCAACTAGCC	ATAAAATAGA	CAACTTTAGT	CTTTAAACA	TTTAATAAAA
3563	3573	3583	3593	3603
TAAATGCAAA	ATATAGACTC	CTTAACTAAA	CTGACTATCT	ATGGAGCCTC
3613	3623	3633	3643	3653
TAATTGATAA	AGATGGAAGT	CGGGACAAGA	CCACGACATC	CTGACTAAAC
3663	3673	3683	3693	3703
TGAGAAGTAA	ATAAAATCCC	CCGGAAAAAA	AGGAGCCTCA	CCATGGCTAA
3713	3723	3733	3743	3753
CTCGAAGTCC	GGGATATATC	AATGAAGCTC	CTGTTGATGA	TCTTGAAGAC
3763	3773	3783	3793	3803
ATGTCTCTGC	ATCATCAAAA	AGATGCAGGC	CAAATGGCTC	AGTACGTAAA
3813	3823	3833	3843	3853
ATGTACGAGT	ATGTAAGGGA	AATTCTAAAG	TATAACATAA	GCTTGATACT
3863	3873	3883	3893	3903
TGAATAAAAG	GAAACATACT	TACCTCTTTT	CAACTCAACT	CAAATTAAGA
3913	3923	3933	3943	3953
ATAAGATACT	CAACTCAAAG	ATTAGGTATT	CAACGCAAAT	ATGGCACTCT
3963	3973	3983	3993	4003
ACTCAATGAA	GTACAAATTA	ACTCAGGATA	CTCGACTTAA	GATACTCAAC
4013	4023	4033	4043	4053
TCCCGACACT	CAACTGAACT	CATTTCAATA	TAAAGCAGCT	TAAAACAAGT
4063	4073	4083	4093	4103
TCAGTATAAA	GTAAAGTTGT	TTAAAAACAT	GATGTCAACT	CTGTGTGTAT
4113	4123	4133	4143	4153
AATAAGGGAT	ACAACATAAC	TTTGAAATGT	ATATAAAAAT	ACAATTAAC

FIGURE 7D

4163	4173	4183	4193	4203
GATGTATATA	AAAATACATT	AATCTATGGG	AGATTCTCTA	ACCGACAACC
4213	4223	4233	4243	4253
ATCACTTAAG	GGCTAAGATG	ATGATATAGC	GATCTACCGC	ACGCTGCCAT
4263	4273	4283	4293	4303
CGCATCTTAT	ACCCGGCCAA	AGGTATAAGA	CCTGAACTGC	CTAATGAATC
4313	4323	4333	4343	4353
CACTAATAAA	CTGTTAAAAG	GAATCATCTA	AAAAGTATGA	CCCTTTTCTA
4363	4373	4383	4393	4403
CCCATAGTGG	CTAACATGGT	TTATGGGGGC	TGTGAGTTAT	CTGAACTCTC
4413	4423	4433	4443	4453
CCCCATATCG	GTGCTCAATA	CTACTCCAAA	AAATATACTG	CTCTTATGTT
4463	4473	4483	4493	4503
TAAAAACATA	CTGATTCTGT	GGTTTGAAAT	TATTGCTTAA	AGCTTAGATT
4513	4523	4533	4543	4553
TTTGAAAAGC	TCTCTTTTGA	AAATCGTAGT	TTCCTTTTTC	TTCTATTAAA
4563	4573	4583	4593	4603
GCTAGACATA	GGCTATGTAG	AACTCTAGCT	TACCTTCCTT	CTCAAAAGTT
4613	4623	4633	4643	4653
TGAAAACATT	TGCTTAGATT	CTTAGGGACT	ACTTAGTTCC	CTTGTTGGAA
TTC				

FIGURE 7E

PG GENOMIC

10	20	30	40	50
AAGCTTCTTA	AAAAGGCAAA	TTGATTAATT	TGAAGTCAAA	ATAATTAATT
60	70	80	90	100
ATAACAGTGG	TAAAGCACCT	TAAGAAACCA	TAGTTTGAAA	GGTTACCAAT
110	120	130	140	150
GCGCTATATA	TTAATCAACT	TGATAATATA	AAAAAAATTT	CAATTCGAAA
160	170	180	190	200
AGGGCCTAAA	ATATTCTCAA	AGTATTTCGAA	ATGGTACAAA	ACTACCATCC
210	220	230	240	250
GTCCACCTAT	TGACTCCAAA	ATAAAATTAT	TATCCACCTT	TGAGTTTAAA
260	270	280	290	300
ATTGACTACT	TATATAACAA	TTCTAAATTT	AAACTATTTT	AATACTTTTA
310	320	330	340	350
AAAATACATG	GCGTTCAAAT	ATTTAATATA	ATTTAATTTA	TGAATATCAT
360	370	380	390	400
TTATAAACCA	ACCAACTACC	AACTCATTA	TCATTAAATC	CCACCCAAAT
410	420	430	440	450
TCTACTATCA	AAATTGTCCT	AAACACTACT	AAAACAAGAC	GAAATTGTTC
460	470	480	490	500
GAGTCCGAAT	CGAAGCACCA	ATCTAATTTA	GGTTGAGCCG	CATATTTAGG
510	520	530	540	550
AGGACACTTT	CAATAGTATT	TTTTTCAAGC	ATGAATTGGA	AATTTAAGAT
560	570	580	590	600
TAATGGTAAA	GAAGTAGTAC	ATCCCGAATT	AATTCATGCC	TTTTTTAAAT
610	620	630	640	650
ATAATTATAT	AAATATTTAT	GATTTGTTTT	AAATATTAAA	ACTTGAATAT
660	670	680	690	700
ATTATTTTTT	TAAAAATTAT	CTATTAAGTA	CCATCACATA	ATTGAGACGA
710	720	730	740	750
AGGAATAATT	AAGATGAACA	TAGTGTTTAA	TTAGTAATGG	ATGGGTTAGTA

FIGURE 8A

760	770	780	790	800
AATTTATTTA	TAAATTATAT	CAATAAGTTA	AATTATAACA	AATATTTGAG
810	820	830	840	850
CGCCATGTAT	TTTAAAAAAT	ATTAAATAGT	TTGAATTTAA	AACCGTTAGA
860	870	880	890	900
TAAATGGTCA	ATTTTGAACC	CAAAAGTGGA	TGAGAAGGGT	ATTTTAGAGC
910	920	930	940	950
CAATAGGRGG	ATGAGAAGGA	TATTTTGAAG	CCAATATGTG	ATGGATGAAG
960	970	980	990	1000
GATAATTTTG	TATCATTTCT	AATACTTTAA	AGATATTTTA	GGTCATTTTC
1010	1020	1030	1040	1050
CCTTCTTTAG	TTTATAGACT	ATAGTGTTAG	TTCATCGAAT	ATCATCTATT
1060	1070	1080	1090	1100
ATTTCCGTCT	TAAATTATTT	TTTATTTTAT	AAATTTTTTA	AAAATAAATT
1110	1120	1130	1140	1150
ATTTTTTCCA	TTTAACTTTG	ATTGTAATTA	ATTTTTTAAA	ATTACCAACA
1160	1170	1180	1190	1200
TATAAATAAA	ATTAATATTT	AACAAAGAAT	TGTAACATAA	TATTTTTTTA
1210	1220	1230	1240	1250
ATTATTCAAA	ATAAATATTT	TTAAACATCA	TATAAAAGAA	ATACGACAAA
1260	1270	1280	1290	1300
AAAATTGAGA	CGGGAGAAGA	CAAGCCAGAC	AAAAATGTCC	AAGAAACTCT
1310	1320	1330	1340	1350
TTCGTCTAAA	TATCTCTCAT	CCAAACTAAT	ATAATACCCA	TTATAATTAA
1360	1370	1380	1390	1400
CCATATTGAC	CAACTCAAAC	CCCTTAAAT	CTATAAATAG	ACAAACCCTT
1410	1420	1430	1440	1450
CCCATACCTC	TTATCATAAA	AAAAATAATA	ATCTTTTTC	ATAGACAAGT
1460	1470	1480	1490	1500
TTAAAAACCA	TACCATATAA	CAATATATCA	TGGTTATCCA	AAGGAATAGT

FIGURE 8B

1510 1520 1530 1540 1550
 ATTCTCCTTC TCATTATTAT TTTTGCTTCA TCAATTTCAA CTTGTAGAAG
 1560 1570 1580 1590 1600
 CAATGTTATT GATGACAATT TATTCAAACA AGTTTATGAT AATATTCTTG
 1610 1620 1630 1640 1650
 AACAGAATT TGCTCATGAT TTTCAAGCTT ATCTTTCTTA TTTGAGCAAA
 1660 1670 1680 1690 1700
 AATATTGAAA GCAACAATAA TATTGACAAG GTTGATAAAA ATGGGATTAA
 1710 1720 1730 1740 1750
 AGTGATTAAT GTACTTAGCT TTGGAGCTAA GGGTGATGGA AAAACATATG
 1760 1770 1780 1790 1800
 ATAATATTGT AAGTATTTAA ATATTGGAAT ATATTTGTGG GGATGAAAAT
 1810 1820 1830 1840 1850
 GATAGAGAAT ATAAGAATTA TTTGGAAGGA TGAAAAGTTA TATTTTATAA
 1860 1870 1880 1890 1900
 AGTAGAAAAT TATTTTCTCG TTTTLAGTAA TTAAAGGTGA AAAATGAGTT
 1910 1920 1930 1940 1950
 TTCTCGTAAG CGAGGAAAGT CATTTTCCAT GGAAGTGTAT TTTTTTTTAA
 1960 1970 1980 1990 2000
 CTTTTAATAA CGTCATAGTA TTTGCTATAC TCAAGAATAA GACACTATTA
 2010 2020 2030 2040 2050
 TTGATGTTTA GTGCTCGAAA AGAAATTGAT AGTAATTTTG CTAATATAAC
 2060 2070 2080 2090 2100
 TATCAATTTC TTATATGTAT ATTTTTC AACAAATAACA AAGCGTAATC
 2110 2120 2130 2140 2150
 CAATAAGTGG GCCTCTAGAA TAAAGAGTAA GTTCTATTAA TTCTTAACCT
 2160 2170 2180 2190 2200
 TATTTAATTT TATGGAAACC TCGACAAAAC GACAATGCTC AACTTATATT
 CGAATTC

FIGURE 8C

65510 1982260

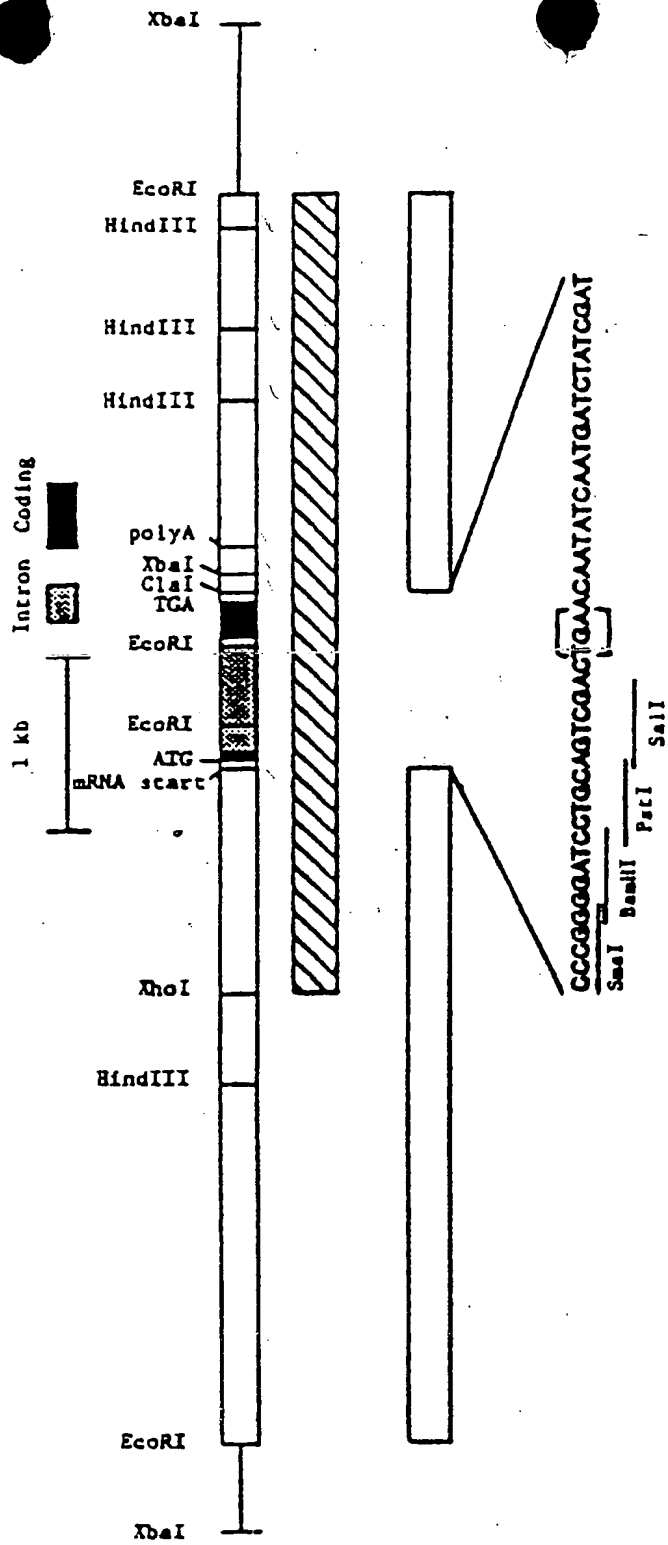


FIGURE 9

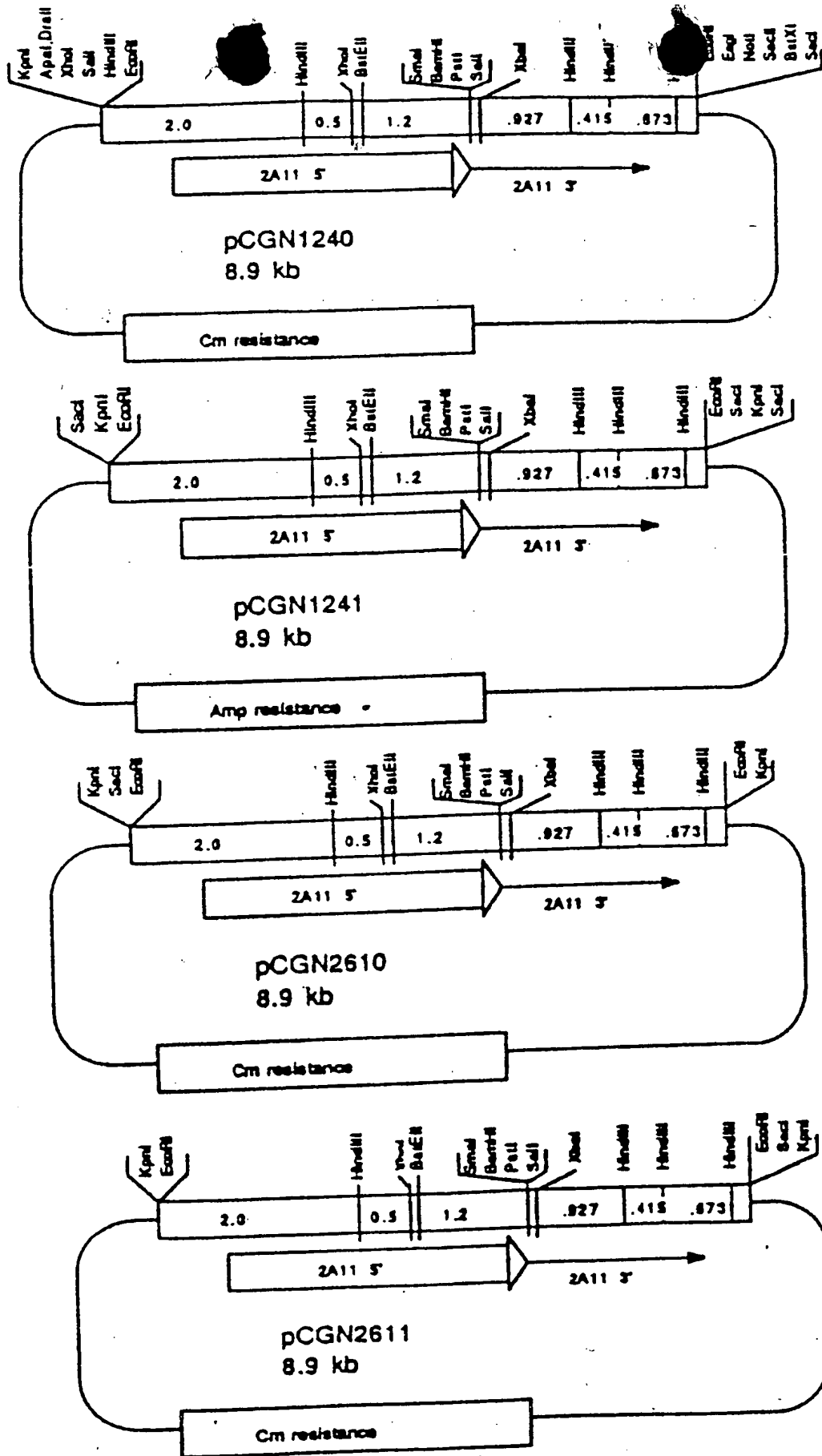


FIGURE 10